```
1
GATCATTAAATAAATCAAGGTTAGTTAGCTTGAAAGATATAAATATATTCCAAAATTCCA
61
AAAAGTAATTGGCATAGTGACAAAAACTATTGCTCCCCTGCTTTAGAAATAATTTATTTT
121
TAATTTAATATTAAAAGTAAACTGAAGAATCTAGTTATATTTAAAAAGTAAAGGTTGCAT
181
TTTAACTAAATTATGTTAAACTACTGTTATGCGATGAGTCGATATGTGGTTTTACCACTA
241
TTGCGCAGGGAGATTATAAACGCAGGAGCGGATCTTGATAAGTTGTGTGAACCTTCTTGT
301
CACACTTGAAAAGGTGCCCTTAGCTTACTACTACTTGTAATTTCTTACAAATTGTGGTAA
361
GTAGCTGAAAAGCAAAAAAGAAAGAACCAGTTTGGTTCTTTCTTTTTTGCATAAATAAGT
421
CACAATTTCCTTCTTAAAATTATGTCTTTACTTAACTTTAATTGAATATGCTACCATCAC
481
ATTCTTTGTAAAATTTTTAAATAATCTAGTTTCTGATGGTTTAGATGAAGTATTAAAAAT
541
ATACTATTACCTCATTGTAAATCTTAATGTTAGTATGACTATCTATCATGCTTTATAATA
601
TTAAAGGAAAATTTAAAAATATCATGTTTTAGATATCAACTATTTAATTTTAAACATACA
661
AATTAATAATAAATTGCAACTAAATAATAAATTATCTTGACATAACTTATAAAATGTTTT
721
AATATATAATCTAAATAAAAGTAATAATAAAATGACTTTTAAAATTTAAAAAAAGTAAGG
781                                                          RBS
AGAAAATTAATTGTTCAATAAAATAGGTTTTAGAACTTGGAAATCAGGAAAGCTTTGGCT
841        M  F  N  K  I  G  F  R  T  W  K  S  G  K  L  W  L
TTATATGGGAGTGCTAGGATCAACTATTATTTTAGGATCAAGTCCTGTATCTGCTATGGA
  Y  M  G  V  L  G  S  T  I  I  L  G  S  S  P  V  S  A  M  D
901                    Repeat 1 (SEQ ID 21)
TAGTGTTGGAAATCAAAGTCAGGGCAATGTTTTAGAGCGTCGTCAACGTGATGCAGAAAA
  S  V  G  N  Q  S  Q  G  N  V  L  E  R  R  Q  R  D  A  E  N
961          Repeat 2 (SEQ ID 22)                Repeat 3 (SEQ ID 23)
CAGAAGCCAAGGCAATGTTCTAGAGCGTCGTCAACGCGATGTTGAGAATAAGAGCCAAGG
  R  S  Q  G  N  V  L  E  R  R  Q  R  D  V  E  N  K  S  Q  G
1021                                Repeat 4 (SEQ ID 24)
CAATGTTTTAGAGCGTCGTCAACGTGATGCGGAAAACAAGAGCCAAGGCAATGTTTTAGA
  N  V  L  E  R  R  Q  R  D  A  E  N  K  S  Q  G  N  V  L  E
1081                  Repeat 5 (SEQ ID 25)
GCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGGCAATGTTCTAGAGCGTCGTCAACG
  R  R  Q  R  D  A  E  N  R  S  Q  G  N  V  L  E  R  R  Q  R
1141        Repeat 6 (SEQ ID 26)
TGATGCAGAAAACAGAAGCCAAGGCAATGTTCTAGAGCGTCGTCAACGCGATGCAGAAAA
```

Fig. 1-1

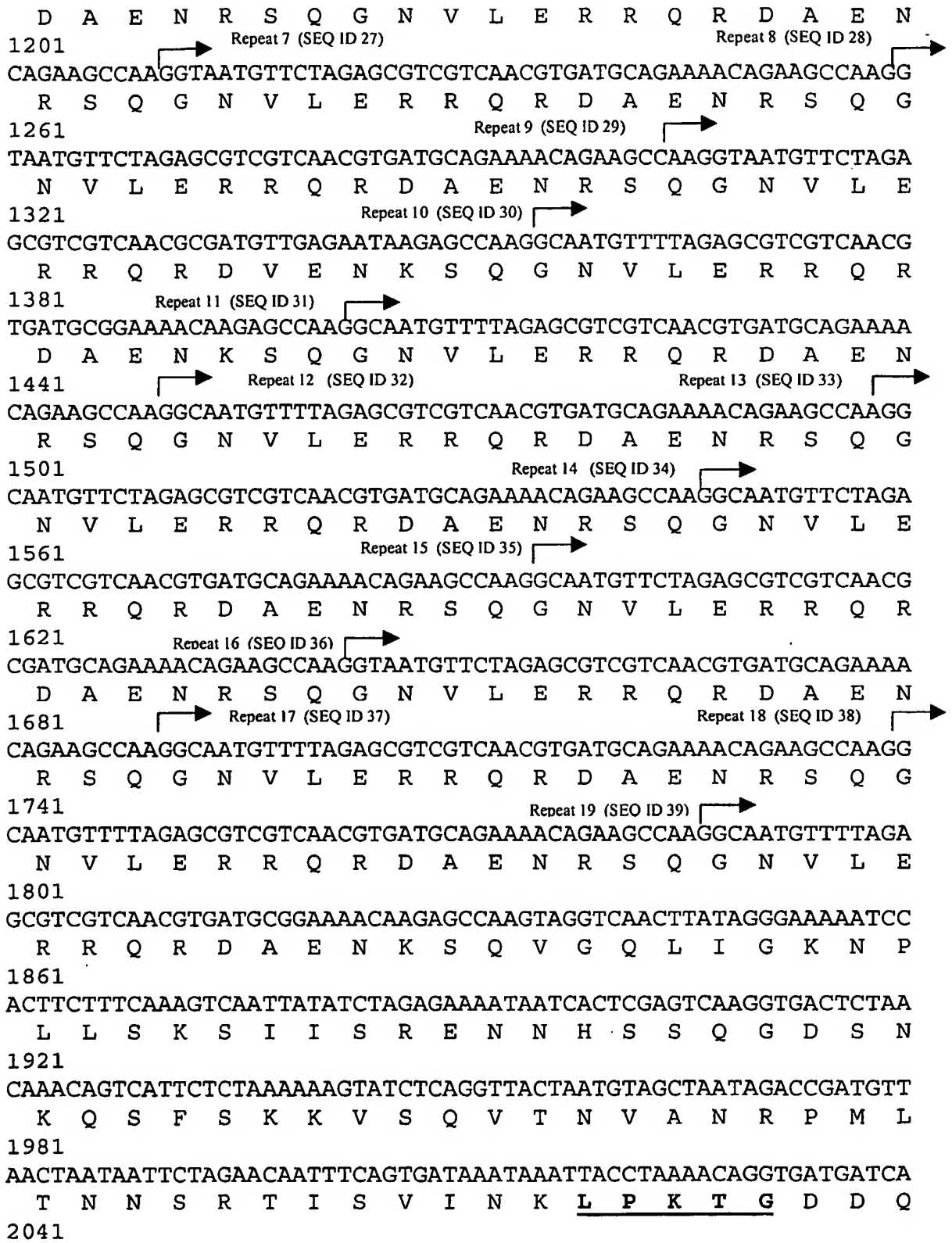

D A E N R S Q G N V L E R R Q R D A E N
1201
Repeat 7 (SEQ ID 27)
Repeat 8 (SEQ ID 28)
CAGAAGCCAAGGTAATGTTCTAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGG
R S Q G N V L E R R Q R D A E N R S Q G
1261
Repeat 9 (SEQ ID 29)
TAATGTTCTAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGGTAATGTTCTAGA
N V L E R R Q R D A E N R S Q G N V L E
1321
Repeat 10 (SEQ ID 30)
GCGTCGTCAACGCGATGTTGAGAATAAGAGCCAAGGCAATGTTTTAGAGCGTCGTCAACG
R R Q R D V E N K S Q G N V L E R R Q R
1381
Repeat 11 (SEQ ID 31)
TGATGCGGAAAACAAGAGCCAAGGCAATGTTTTAGAGCGTCGTCAACGTGATGCAGAAAA
D A E N K S Q G N V L E R R Q R D A E N
1441
Repeat 12 (SEQ ID 32)
Repeat 13 (SEQ ID 33)
CAGAAGCCAAGGCAATGTTTTAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGG
R S Q G N V L E R R Q R D A E N R S Q G
1501
Repeat 14 (SEQ ID 34)
CAATGTTCTAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGGCAATGTTCTAGA
N V L E R R Q R D A E N R S Q G N V L E
1561
Repeat 15 (SEQ ID 35)
GCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGGCAATGTTCTAGAGCGTCGTCAACG
R R Q R D A E N R S Q G N V L E R R Q R
1621
Repeat 16 (SEQ ID 36)
CGATGCAGAAAACAGAAGCCAAGGTAATGTTCTAGAGCGTCGTCAACGTGATGCAGAAAA
D A E N R S Q G N V L E R R Q R D A E N
1681
Repeat 17 (SEQ ID 37)
Repeat 18 (SEQ ID 38)
CAGAAGCCAAGGCAATGTTTTAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGG
R S Q G N V L E R R Q R D A E N R S Q G
1741
Repeat 19 (SEQ ID 39)
CAATGTTTTAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGGCAATGTTTTAGA
N V L E R R Q R D A E N R S Q G N V L E
1801
GCGTCGTCAACGTGATGCGGAAAACAAGAGCCAAGTAGGTCAACTTATAGGGAAAAATCC
R R Q R D A E N K S Q V G Q L I G K N P
1861
ACTTCTTTCAAAGTCAATTATATCTAGAGAAAATAATCACTCGAGTCAAGGTGACTCTAA
L L S K S I I S R E N N H S S Q G D S N
1921
CAAACAGTCATTCTCTAAAAAAGTATCTCAGGTTACTAATGTAGCTAATAGACCGATGTT
K Q S F S K K V S Q V T N V A N R P M L
1981
AACTAATAATTCTAGAACAATTTCAGTGATAAATAAATTACCTAAAACAGGTGATGATCA
T N N S R T I S V I N K L P K T G D D Q
2041

Fig. 1-2

```
AAATGTCATTTTTAAACTTGTAGGTTTTGGTTTAATTTTGTTAACAAGTCGCTGCGGTTT
  N  V  I  F  K  L  V  G  F  G  L  I  L  L  T  S  R  C  G  L
2101
GAGACGCAATGAAAATTAAGTATAATCAATCATTTAGTAACTATATATAATGATATATGC
  R  R  N  E  N  *
2161 ————————————→                ←————————————
AATCAATAAAAAGGAATCGGATACGAGATTCCTTTTTATAATTAGGTTGGTTAGGGTGAC
2221
TTTTTTCATTTGGCTATTCTTGAAAGTTTATAAAAATGTAGTTATAATAGTCACATTAAA
2281
ATGTTTTGAAAATATTGATGAACAACATCAACAAATAGAGGTCATTATATGGGATATACC
2341
GTTGCTATCGTAGGTGCTACAGGTGCCGTAGGAACACAAATGATTCGTCAATTAGAACAA
2401
TCGAATTTACCAATAGAACAAGTGAAACTTTTATCATCAAGTCGCTCAGCAGGTAAAATT
2461
TTACATTTTAAAGATGAGGCTATACGTGTTGAAGAGACAACAAAAGAATCATTTTACGAT
2521
GTTGATATTGCCTTGTTTTCAGCTGGTGGATC
```

Fig. 1-3

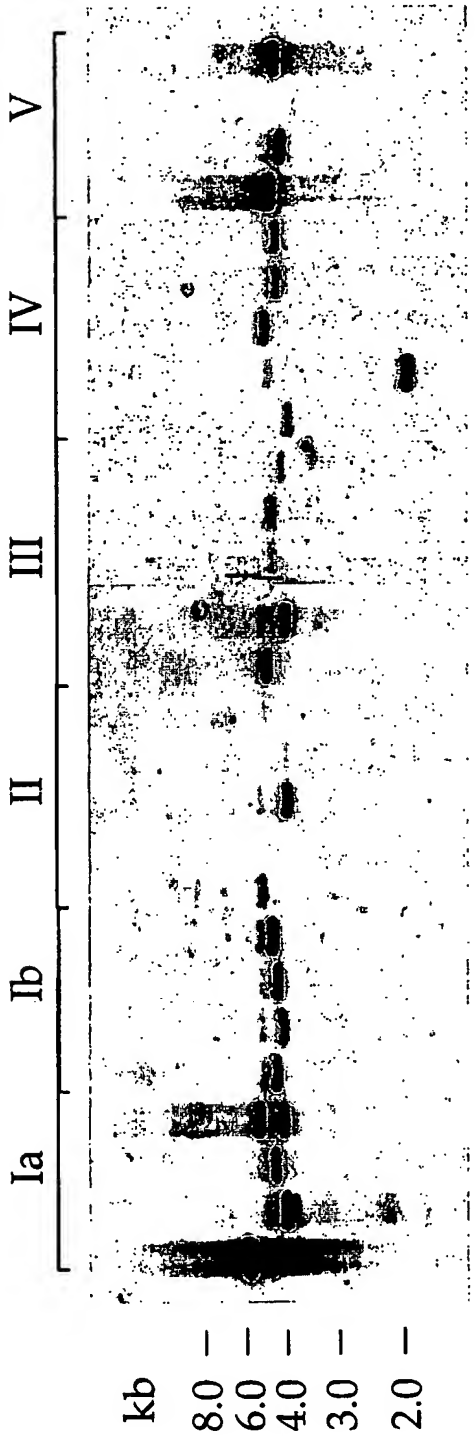


Fig. 2

1
GCATAAATAAGTCACAATTTCCTTCTTAAAATTATGTCTTTACTTAACTTTAATTGAATA
61
TGCTACCATCACATTCTTTGTAAAATTTTTAAATAATCTAGTTTCTGATGGTTTAGATGA
121
AGTATTAAAAATATACTATTACCTCATTGTAAATCTTAATGTTAGTATGACTATCTATCA
181
TGCTTTATAATATTAAAGGAAAATTTAAAAATATCATGTTTTAGATATCAACTATTTAAT
241
TTTAAACATACAAATTAATAATAAATTGCAACTAAATAATAAATTATCTTGACATAACTT
301
ATAAAATGTTTTAATATATAATCTAAATAAAAGTAATAATAAAATGACTTTTAAAATTTA
361
AAAAAAGTAAGGAGAAAATTAATTGTTCAATAAAATAGGTTTTAGAACTTGGAAATCAGG
421 RBS *M F N K I G F R T W K S G*
AAAGCTTTGGCTTTATATGGGAGTGCTAGGATCAACTATTATTTTAGGATCAAGTTCTGT
K L W L Y M G V L G S T I I L G S S S V
481 Repeat 1 (SEQ ID 40)
ATCTGCTATGGATAGTGTTGGAAATCAAAGTCAGGGCAATGTTTTAGAGCGTCGTCAACG
S A M D S V G N Q S Q G N V L E R R Q R
541 Repeat 2 (SEQ ID 41)
CGATGCAGAAAACAGAAGCCAAGGCAATGTTTTAGAGCGTCGTCAACGTGATGCAGAAAA
D A E N R S Q G N V L E R R Q R D A E N
601 Repeat 3 (SEQ ID 42) Repeat 4 (SEQ ID 43)
CAGAAGCCAAGGCAATGTTTTAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGG
R S Q G N V L E R R Q R D A E N R S Q G
661 Repeat 5 (SEQ ID 44)
TAATGTTCTAGAGCGTCGTCAACGCGATGTTGAAAATAAAAGCCAAGGCAATGTTTTAGA
N V L E R R Q R D V E N K S Q G N V L E
721 Repeat 6 (SEQ ID 45)
GCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGGTAATGTTCTAGAGCGTCGTCAACG
R R Q R D A E N R S Q G N V L E R R Q R
781 Repeat 7 (SEQ ID 46)
CGATGTTGAAAATAAAAGCCAAGGCAATGTTTTAGAGCGTCGTCAACGTGATGCAGAAAA
D V E N K S Q G N V L E R R Q R D A E N
841 Repeat 8 (SEQ ID 47) Repeat 9 (SEQ ID 48)
CAGAAGCCAAGGTAATGTTCTAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGG
R S Q G N V L E R R Q R D A E N R S Q G
901 Repeat 10 (SEQ ID 49)
CAATGTTTTAGAGCGTCGTCAACGCGATGCAGAAAACAGAAGCCAAGGCAATGTTCTAGA
N V L E R R Q R D A E N R S Q G N V L E

Fig. 3-1

961 Repeat 11 (SEQ ID 50)
GCGTCGTCAACGTGATGCTGAAAACAAAAGCCAAGGCAATGTTTTAGAGCGTCGTCAACG
R R Q R D A E N K S Q G N V L E R R Q R
1021 Repeat 12 (SEQ ID 51)
TGATGCAGAAAACAGAAGCCAAGGCAATGTTTTAGAGCGTCGTCAACGTGATGCTGAAAA
D A E N R S Q G N V L E R R Q R D A E N
1081 Repeat 13 (SEQ ID 52) Repeat 14 (SEQ ID 53)
CAGAAGCCAAGGCAATGTTTTAGAGCGTCGTCAACGCGATGCAGAAAACAGAAGCCAAGG
R S Q G N V L E R R Q R D A E N R S Q G
1141 Repeat 15 (SEQ ID 54)
TAATGTTCTAGAGCGTCGTCAACGTGATGCGGAAAACAAGAGCCAAGGCAATGTTTTAGA
N V L E R R Q R D A E N K S Q G N V L E
1201 Repeat 16 (SEQ ID 55)
GCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGGCAATGTTTTAGAGCGTCGTCAACG
R R Q R D A E N R S Q G N V L E R R Q R
1261 Repeat 17 (SEQ ID 56)
CGATGTTGAGAATAAGAGCCAAGGCAATGTTTTAGAGCGTCGTCAACGTGATGCGGAAAA
D V E N K S Q G N V L E R R Q R D A E N
1321
CAAGAGCCAAGTAGGTCAACTTATAGGGAAAAATCCACTTCTTTCAAAGTCAATTATATC
K S Q V G Q L I G K N P L L S K S I I S
1381
TAGAGAAAATAATCACTCTAGTCAAGGTGACTCTAACAAACAGTCATTCTCTAAAAAAGT
R E N N H S S Q G D S N K Q S F S K K V
1441
ATCTCAGGTTACTAATGTAGCTAATAGACCGATGTTAACTAATAATTCTAGAACAATTTC
S Q V T N V A N R P M L T N N S R T I S
1501
AGTGATAAATAAATTACCTAAAACAGGTGATGATCAAAATGTCATTTTTAAACTTGTAGG
V I N K **L P K T G** D D Q N V I F K L V G
1561
TTTTGGTTTAATTTTGTTAACAAGTCGCTGCGGTTTGAGACGCAATGAAAATTAAGTATA
F G L I L L T S R C G L R R N E N *
1621
ATCAATCATTTAGTAACTATATATAATGATATATGCAATCAATAAAAAGGAATCGGATAC

GAGATTCCTTTTTATAATTAGGTTGGTTAGGGTGACTTTTTTCATTTGGCTATTCTTGAA
1741 1761 1781
AGTTTATAAAAATGTAGTATAATAGTCACATTAAAATGTTTTGAAAATATTGATGAACAA
1801
CATCAACAAATAGAGGTCAT

Fig. 3-2

1
GCATAAATAAGTCACAATTTCCTTCTAAAAATTATGTCTTTACTTAACTTTAATTGAATA
61
TGCTACCATCACATTCTTTGTAAAATTTTTAAATAATCTAGTTTCTGATGGTTTAGATGA
121
AGTATTAAAAATATACTATTATCTCATTGTAAATCCTAATGTTAGTATGACTATCTATCA
181
TGTTTTATAATATTGAAGGAAAATTTAAAAATATCATGTTTTAGATATCAACTATTTAAT
241
TTTAAACATACAAATTAATAATAAATTGCAATTAAATAACAAATTACCTTGACATAAATT
301
ATAAAATGTTTTAATATATATAATCTAAATAAAAATAATAATAAAATGACTTTTAAAATT
361
TAAAAAAAGTAAGGAGAAAATTAATTGTTCAATAAAATAGGTTTTAGAACTTGGAAATCA
421 RBS *M F N K I G F R T W K S*
GGAAAGCTTTGGCTTTATATGGGAGTGCTAGGATCAACTATTATTTTAGGATCAAGTCCT
G K L W L Y M G V L G S T I I L G S S P
481 Repeat 1 (SEQ ID 57)
GTATCTGCTATGGATAGTGTTGGAAATCAAAGTCAAGGTAATGTTCTAGAGCGTCGTCAA
V S A M D S V G N Q S Q G N V L E R R Q
541 Repeat 2 (SEQ ID 58)
CGTGATGCGGATAACAAGAGCCAAGGCAATGTTCTAGAACGTCGTCAACGCGATGTAGAA
R D A D N K S Q G N V L E R R Q R D V E
601 Repeat 3 (SEQ ID 59)
AACAGAAGCCAAGGCAATGTTCTAGAGCGTCGTCAACGCGATGCGGATAACAAGAGCCAA
N R S Q G N V L E R R Q R D A D N K S Q
Repeat 4 (SEQ ID 60) Repeat 5 (SEQ ID 61)
GGCAATGTTTTAGAGCGCCGCCAACGCGATGCAGAAAACAAAAGTCAGGGCAATGTTCTA
G N V L E R R Q R D A E N K S Q G N V L
721 Repeat 6 (SEQ ID 62)
GAACGTCGTCAACGTGATGTTGAGAATAAGAGCCAAGGCAATGTTCTAGAGCGTCGCCAA
E R R Q R D V E N K S Q G N V L E R R Q
781 Repeat 7 (SEQ ID 63)
CGTGATGCAGAAAACAAAAGTCAGGGTAATGTTCTAGAGCGTCGTCAACGCGATGCAGAT
R D A E N K S Q G N V L E R R Q R D A D
841 Repeat 8 (SEQ ID 64)
AACAAGAGCCAAGGTAATGTTCTAGAACGTCGTCAACGCGATGTGGAAAACAAAAGTCAG
N K S Q G N V L E R R Q R D V E N K S Q
Repeat 9 (SEQ ID 65) Repeat 10 (SEQ ID 66)
GGCAATGTTCTAGAACGTCGTCAACGTGATGTTGAGAATAAGAGCCAAGGCAATGTTCTA
G N V L E R R Q R D V E N K S Q G N V L
961 Repeat 11 (SEQ ID 67)
GAGCGTCGCCAACGTGATGCAGAAAACAAAAGTCAGGGTAATGTTCTAGAGCGTCGTCAA
E R R Q R D A E N K S Q G N V L E R R Q

Fig. 4-1

1021 Repeat 12 (SEQ ID 68)

CGCGATGCAGATAACAAGAGCCAAGGTAATGTTCTAGAACGTCGTCAACGCGATGTGGAA

R D A D N K S Q G N V L E R R Q R D V E

1081 Repeat 13 (SEQ ID 69)

AACAAAAGTCAGGGCAATGTTCTAGAGCGTCGCCAACGTGATGTTGAGAACAAGAGCCAA

N K S Q G N V L E R R Q R D V E N K S Q

1141

GTAGGTCAACTTATAGGGAAAAATCCACTTCTTTCAAAGTCAACTATATCTAGAGAAAAT

V G Q L I G K N P L L S K S T I S R E N

1201

AATCACTCTAGTCAAGGTGACTCTAACAAACAGTCATTCTCTAAAAAAGTATCTCAGGTT

N H S S Q G D S N K Q S F S K K V S Q V

1261

ACTAATGTAGCTAATAGACCAATGTTAACTAATAATTCTAGAACAATTTCAGTGATAAAT

T N V A N R P M L T N N S R T I S V I N

1321

AAATTACCTAAAACAGGTGATGATCAAAATGTCATTTTTAAACTTGTAGGTTTTGGTTTA

K **L P K T G** D D Q N V I F K L V G F G L

1381

ATTTTGTTAACAAGTCGCTGCGGTTTGAGACGCAATGAAAATTAAGTATAATCAATCATT

I L L T S R C G L R R N E N *

1441

TAGTAACTATTATAATGATATATGCAATCAATAAAAAGGAATCGGATACAAGATTCCTTT

TTATAATTAGGTTGGTTAGGGTGACTTTTTCATTTGGCTATTCTTGAAAGTTTATAAAAA

1561

TGTAGTATAATAGTCACATTAAAATGTTTTGAAAATATTGATGAACAACATCAACAAATA

1621

GAGGTCAT

Fig. 4-2

```
1
GCATAAATAAGTCACCAATTTCCCTTCTTAAAATTATGTCTTTACTTAACTTTAATTGAA
61
TATGCTACCATCACATTCTTTGTAAAATTTTTAAATAATCTAGTTTCTGATGGTTTAGAT
121
GAAGTATTAAAAATATACTATTACCTCATTGTAAATCTTAATGTTAGTATGACTATCTAT
181
CATGCTTTATAATATTAAAGGAAAATTTAAAAATATCATGTTTTAGATATCAACTATTTA
241
ATTTTAAACATACAAATTAATAATAAATTGCAACTAAATAATAAATTATCTTGACATAAC
301
TTATAAAATGTTTTAATATATAATCTAAATAAAAGTAATAATAAAATGACTTTTAAAATT
361
TAAAAAAAGTAAGGAGAAAATTAATTGTTCAATAAAATAGGTTTTAGAACTTGGAAATCA
421          RBS          M  F  N  K  I  G  F  R  T  W  K  S
GGAAAGCTTTGGCTTTATATGGGAGTGCTAGGATCAACTATTATTTTAGGATCAAGTCCT
 G  K  L  W  L  Y  M  G  V  L  G  S  T  I  I  L  G  S  S  P
481                                Repeat 1 (SEQ ID 70)
GTATCTGCTATGGATAGTGTTGGAAATCAAAGTCAGGGCAATGTTTTAGAGCGTCGTCAA
 V  S  A  M  D  S  V  G  N  Q  S  Q  G  N  V  L  E  R  R  Q
541                Repeat 2 (SEQ ID 71)
CGCGATGCAGAAAACAGAAGCCAAGGTAATGTTCTAGAGCGTCGTCAACGCGATGCAGAA
 R  D  A  E  N  R  S  Q  G  N  V  L  E  R  R  Q  R  D  A  E
601          Repeat 3 (SEQ ID 72)
AACAGAAGCCAAGGTAATGTTCTAGAGCGTCGTCAACGTGATGCGGAAAACAAGAGCCAA
 N  R  S  Q  G  N  V  L  E  R  R  Q  R  D  A  E  N  K  S  Q
661
GTAGGTCAACTTATAGGGAAAAATCCACTTCTTTCAAAGTCAATTATATCTAGAGAAAAT
 V  G  Q  L  I  G  K  N  P  L  L  S  K  S  I  I  S  R  E  N
721
AATCACTCTAGTCAAGGTGACTCTAACAAACAGTCATTCTCTAAAAAAGTATCTCAGGTT
 N  H  S  S  Q  G  D  S  N  K  Q  S  F  S  K  K  V  S  Q  V
781
ACTAATGTAGCTAATAGACCGATGTTAACTAATAATTCTAGAACAATTTCAGTGATAAAT
 T  N  V  A  N  R  P  M  L  T  N  N  S  R  T  I  S  V  I  N
841
AAATTACCTAAAACAGGTGATGATCAAAATGTCATTTTTAAACTTGTAGGTTTTGGTTTA
 K  L  P  K  T  G  D  D  Q  N  V  I  F  K  L  V  G  F  G  L
901
ATTTTGTTAACAAGTCGCTGCGGTTTGAGACGCAATGAAAATTAAGTATAATCAATCATT
 I  L  L  T  S  R  C  G  L  R  R  N  E  N  *
961
TAGTAACTATATATAATGATATATGCAATCAATAAAAAGGAATCGGATACGAGATTCCTT

TTTATAATTAGGTTGGTTAGGGTGACTTTTTTCATTTGGCTATTCTTGAAAGTTTATAAA
1081
AATGTAGTATAATAGTCACATTAAAATGTTTTGAAAATATTGATGAACAACATCAACAAA
1141
TAGAGGTCAT
```

Fig. 5

```
1
GCATAAATAAGTCACAATTTCCTTCTTAAAATTATGTCTTTACTTAACTTTAATTGAATA
61
TGCTACCATCACATTCTTTGTAAAATTTTTAAATAATCTAGTTTCTGATGGTTTAGATGA
121
AGTATTAAAAATATACTATTACCTCATTGTAAATCTTAATGTTAGTATGACTATCTATCA
181
TGCTTTATAATATTAAAGGAAAATTTAAAAATATCATGTTTTAGATATCAACTATTTAAT
241
TTTAAACATACAAATTAATAATAAATTGCAACTAAATAATAAATTATCTTGACATAACTT
301
ATAAAATGTTTTAATATATAATCTAAATAAAAGTAATAATAAAATGACTTTTAAAATTTA
361
AAAAAAGTAAGGAGAAAATTAATTGTTCAATAAAATAGGTTTTAGAACTTGGAAATCAGG
421        RBS          M  F  N  K  I  G  F  R  T  W  K  S  G
AAAGCTTTGGCTTTATATGGGAGTGCTAGGATCAACTATTATTTTAGGATCAAGTCCTGT
  K  L  W  L  Y  M  G  V  L  G  S  T  I  I  L  G  S  S  P  V
481                    Repeat 1 (SEQ ID 73)
ATCTGCTATGGATAGTGTTGGAAATCAAAGCCAAGGCAATGTTCTAGAGCGTCGTCAACG
  S  A  M  D  S  V  G  N  Q  S  Q  G  N  V  L  E  R  R  Q  R
541          Repeat 2 (SEQ ID 74)
CGATGCAGAAAACAGAAGCCAAGGTAATGTTTTAGAACGTCGTCAACGCGATGTTGAGAA
  D  A  E  N  R  S  Q  G  N  V  L  E  R  R  Q  R  D  V  E  N
601      Repeat 3 (SEQ ID 75)          Repeat 4 (SEQ ID 76)
CAAGAGCCAAGGTAATGTTTTAGAGCGTCGCCAACGTGATGCGGAAAACAAAAGTCAGGG
  K  S  Q  G  N  V  L  E  R  R  Q  R  D  A  E  N  K  S  Q  G
661                    Repeat 5 (SEQ ID 77)
CAATGTTTTAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGGTAATGTTCTAGA
  N  V  L  E  R  R  Q  R  D  A  E  N  R  S  Q  G  N  V  L  E
721                    Repeat 6 (SEQ ID 78)
GCGTCGTCAACGCGATGTTGAGAATAAGAGCCAAGGCAATGTTCTAGAGCGTCGTCAACG
  R  R  Q  R  D  V  E  N  K  S  Q  G  N  V  L  E  R  R  Q  R
781          Repeat 7 (SEQ ID 79)
CGATGTTGAGAATAAGAGCCAAGGTAATGTTCTAGAGCGTCGTCAACGCGATGTTGAGAA
  D  V  E  N  K  S  Q  G  N  V  L  E  R  R  Q  R  D  V  E  N
841      Repeat 8 (SEQ ID 80)          Repeat 9 (SEQ ID 81)
TAAGAGCCAAGGTAATGTTCTAGAGCGTCGTCAACGTGATGCGGAAAACAAGAGCCAAGG
  K  S  Q  G  N  V  L  E  R  R  Q  R  D  A  E  N  K  S  Q  G
901                    Repeat 10 (SEQ ID 82)
CAATGTTCTAGAGCGTCGTCAACGCGATGCAGAAAACAGAAGCCAAGGTAATGTTTTAGA
  N  V  L  E  R  R  Q  R  D  A  E  N  R  S  Q  G  N  V  L  E
961
GCGTCGCCAACATGATGTTGAGAATAAGAGTCAAGTAGGTCAACTTATAGGGAAAAATCC
  R  R  Q  H  D  V  E  N  K  S  Q  V  G  Q  L  I  G  K  N  P
1021
ACTTTTTTCAAAGTCAACTGTATCTAGAGAAAATAATCACTCTAGTCAAGGTGACTCTAA
  L  F  S  K  S  T  V  S  R  E  N  N  H  S  S  Q  G  D  S  N
1081
```

Fig. 6-1

```
CAAACAGTCATTCTCTAAAAAAGTATCTCAGGTTACTAATGTAGCTAATAGACCGATGTT
  K  Q  S  F  S  K  K  V  S  Q  V  T  N  V  A  N  R  P  M  L
1141
AACTAATAATTCTAGAACAATTTCAGTGATAAATAAATTACCTAAAACAGGTGATGATCA
  T  N  N  S  R  T  I  S  V  I  N  K  L  P  K  T  G  D  D  Q
1201
AAATGTCATTTTTAAACTTGTAGGTTTTGGTTTAATTTTATTAACAAGTCTCTGCGGTTT
  N  V  I  F  K  L  V  G  F  G  L  I  L  L  T  S  L  C  G  L
1261
GAGACGCAATGAAAATTAAGTATAATCAACCATTTAGTAACTATTATAATGATATATGCA
  R  R  N  E  N  *
1321
ATCAATAAAAAAGGAATCGAATACGAGATTCCTTTTTATAATTAGGTTGGTTAGGGTGAC
1381
TTTTTTCATTTGGCTATTCTTGAAAGTTTATAAAAATGTAGTATAATAGTCACATTAAAA
1441
TGTTTTGAAAATATTGATGAACAACATCATCAAATAGAGGTCAT
```

Fig. 6-2

1
GCATAAATAAGTCACAATTTCCTTCTAAAAATTATGTCTTTACTTAACTTTAATTGAATA
61
TGCTACCATCACATTCTTTGTAAAATTTTTAAATAACCTAGTTTCTGATGGTTTAGATGA
121
AGTATTAAAAATATACTATTATCTCATTGTAAATCCTAATGTTAGTATGACTATCTATCA
181
TGTTTTATAATATTGAAGGAAAATTTAAAAATATCATGTTTTAGATATCAACTATTTAAT
241
TTTAAACATACAAATTAATAATAAATTGCAATTAAATAACAAATTACCTTGACATAAATT
301
ATAAAATGATTTAATATATATAATCTAAATAAAAATAATAATAAAATGACTTTTAAAATT
361
TAAAAAAAGTAAGGAGAAAATTAATTGTTCAATAAAATAGGTTTTAGAACTTGGAAATCA
421 RBS *M F N K I G F R T W K S*
GGAAAGCTTTGGCTTTATATGGGAGTGCTAGGATCAACTATTATTTTAGGATCAAGTCCT
G K L W L Y M G V L G S T I I L G S S P
481 Repeat 1 (SEQ ID 83)
GTATCTGCTATGGATAGTGTTGGAAATCAAAGTCAAGGTAATGTTCTAGAGCGTCGCCAA
V S A M D S V G N Q S Q G N V L E R R Q
541 Repeat 2 (SEQ ID 84)
CGTGATGCGGATAACAAGAGCCAAGGTAATGTTTTAGAGCGTCGCCAACGTGATGCAGAT
R D A D N K S Q G N V L E R R Q R D A D
601 Repeat 3 (SEQ ID 85)
AACAAAAGTCAGGGCAATGTTCTAGAACGTCGCCAACGTGATGTTGATAACAAGAGCCAA
N K S Q G N V L E R R Q R D V D N K S Q
Repeat 4 (SEQ ID 86) Repeat 5 (SEQ ID 87)
GGTAACGTTCTAGAGCGTCGCCAACGCGATGCTGATAACAAGAGCCAAGGTAATGTTTTA
G N V L E R R Q R D A D N K S Q G N V L
721 Repeat 6 (SEQ ID 88)
GAGCGCCGCCAACGCGATGCAGATAACAAAAGTCAAGGTAATGTTCTAGAGCGTCGCCAA
E R R Q R D A D N K S Q G N V L E R R Q
781 Repeat 7 (SEQ ID 89)
CGCGATGTTGATAACAAGAGCCAGGGTAATGTTTTAGAGCGTCGCCAACGCGATGCAGAT
R D V D N K S Q G N V L E R R Q R D A D
841 Repeat 8 (SEQ ID 90)
AACAAAAGTCAGGGTAATGTTTTAGAGCGTCGCCAACGCGATGTTGATAACAAAAGCCAA
N K S Q G N V L E R R Q R D V D N K S Q
Repeat 9 (SEQ ID 91) Repeat 10 (SEQ ID 92)
GGTAATGTTTTAGAGCGTCGCCAACGTGATGCTGATAACAAAAGTCAGGGCAATGTTCTA
G N V L E R R Q R D A D N K S Q G N V L
961 Repeat 11 (SEQ ID 93)
GAGCGTCGCCAACGTGATGCGGATAACAAAAGCCAAGGTAATGTTCTAGAGCGTCGCCAA
E R R Q R D A D N K S Q G N V L E R R Q
1021 Repeat 12 (SEQ ID 94)
CGCGATGCGGATAACAAAAGTCAGGGCAATGTTTTAGAGCGTCGCCAACGTGATGCTGAT
R D A D N K S Q G N V L E R R Q R D A D

Fig. 7-1

1081 Repeat 13 (SEQ ID 95)
AACAAAAGTCAAGGTAATGTTCTAGAGCGTCGCCAACGCGATGCAGATAACAAAAGCCAA
N K S Q G N V L E R R Q R D A D N K S Q
Repeat 14 (SEQ ID 96) Repeat 15 (SEQ ID 97)
GGTAATGTTCTAGAGCGTCGCCAACGCGATGCTGATAACAAAAGTCAAGGTAATGTTCTA
G N V L E R R Q R D A D N K S Q G N V L
1201 Repeat 16 (SEQ ID 98)
GAGCGTCGCCAACGTGATGCTGATAACAAGAGCCAAGGCAATGTTCTTGAGCGTCGTCAA
E R R Q R D A D N K S Q G N V L E R R Q
1261 Repeat 17 (SEQ ID 99)
CGCGATGTCGATAACAAAAGTCAGGGTAATGTTTTAGAGCGTCGCCAACGTGATGCGGAT
R D V D N K S Q G N V L E R R Q R D A D
1321 Repeat 18 (SEQ ID 100)
AACAAGAGTCAAGGTAATGTTTTAGAGCGTCGCCAACGCGATGCGGATAACAAGAGCCAA
N K S Q G N V L E R R Q R D A D N K S Q
Repeat 19 (SEQ ID 101) Repeat 20 (SEQ ID 102)
GGTAATGTTTTAGAGCGTCGCCAACGCGATGCGGATAACAAGAGTCAAGGTAATGTTTTA
G N V L E R R Q R D A D N K S Q G N V L
1441 Repeat 21 (SEQ ID 103)
GAGCGTCGCCAACGCGATGCGGATAACAAGAGCCAAGGTAATGTTTTAGAGCGTCGCCAA
E R R Q R D A D N K S Q G N V L E R R Q
1501 Repeat 22 (SEQ ID 104)
CGCGATGCAGATAACAAAAGTCAAGGTAATGTTTTAGAGCGTCGCCAACGCGATGCTGAT
R D A D N K S Q G N V L E R R Q R D A D
1561 Repeat 23 (SEQ ID 105)
AACAAGAGCCAAGGTAATGTTTTAGAGCGTCGTCAACGTGATGCAGATAACAAAAGTCAG
N K S Q G N V L E R R Q R D A D N K S Q
Repeat 24 (SEQ ID 106) Repeat 25 (SEQ ID 107)
GGCAATGTTTTAGAGCGTCGTCAACGTGATGCGGATAACAAGAGCCAAGGTAATGTTTTA
G N V L E R R Q R D A D N K S Q G N V L
1681 Repeat 26 (SEQ ID 108)
GAGCGTCGCCAACGTGATGCGGATAACAAGAGCCAGGGCAATGTTCTAGAACGTCGTCAA
E R R Q R D A D N K S Q G N V L E R R Q
1741 Repeat 27 (SEQ ID 109)
CGTGATGCGGATAACAAGAGCCAAGGTAACGTTTTAGAGCGTCGCCAACGTGATGCGGAT
R D A D N K S Q G N V L E R R Q R D A D
1801 Repeat 28 (SEQ ID 110)
AACAAGAGCCAGGGCAATGTTTTAGAGCGCCGCCAACGCGATGCAGATAACAAAAGTCAA
N K S Q G N V L E R R Q R D A D N K S Q
Repeat 29 (SEQ ID 111) Repeat 30 (SEQ ID 112)
GGTAATGTTCTAGAGCGTCGCCAACGCGATGCAGATAACAAGAGCCAGGGTAATGTTCTA
G N V L E R R Q R D A D N K S Q G N V L
1921
GAGCGTCGCCAACGCGATGCGGAAAACAAAAGTCAAGTAGGTCAACTTATAGGGAAAAAT
E R R Q R D A E N K S Q V G Q L I G K N
1981

Fig. 7-2

```
CCACTTTTTTCAAAGTCAACTGTATCTAGAGAAAATAATCACTCTAGTCAAGGTGACTCT
 P  L  F  S  K  S  T  V  S  R  E  N  N  H  S  S  Q  G  D  S
2041
AACAAACAGTCATTCTCTAAAAAAATATCTCAGGTTACTAATGTAGCTAATGGACCGATG
 N  K  Q  S  F  S  K  K  I  S  Q  V  T  N  V  A  N  G  P  M
2101
TTAACTAATAATTCTAGAACAATTTCAGTGATAAATAAATTACCTAAAACAGGTGATGAT
 L  T  N  N  S  R  T  I  S  V  I  N  K  L  P  K  T  G  D  D
2161
CAAAATGTCATTTTTAAACTTGTAGGTTTTGGTTTAATTTTGTTAACAAGTCTCTGCGGT
 Q  N  V  I  F  K  L  V  G  F  G  L  I  L  L  T  S  L  C  G
2221
TTGAGACGCAATGAAAATTAAGTATAATCAACCATTTAGTAACTATTATAATGATATATG
 L  R  R  N  E  N  *
2281
CAATCAATAAAAAAGGAATCGAATACGAGATTCCTTTTTATAATTAGGTTGGTTAGGGTG
2341                  2361                  2381
ACTTTTTTCATTTGGCTATTCTTGAAAGTTTATAAAAATGTAGTATAATAGTCACATTAA
2401                  2421                  2441
AATGTTTTGAAAATATTGATGAACAACATCATCAAATAGAGGTCAT
```

Fig. 7-3

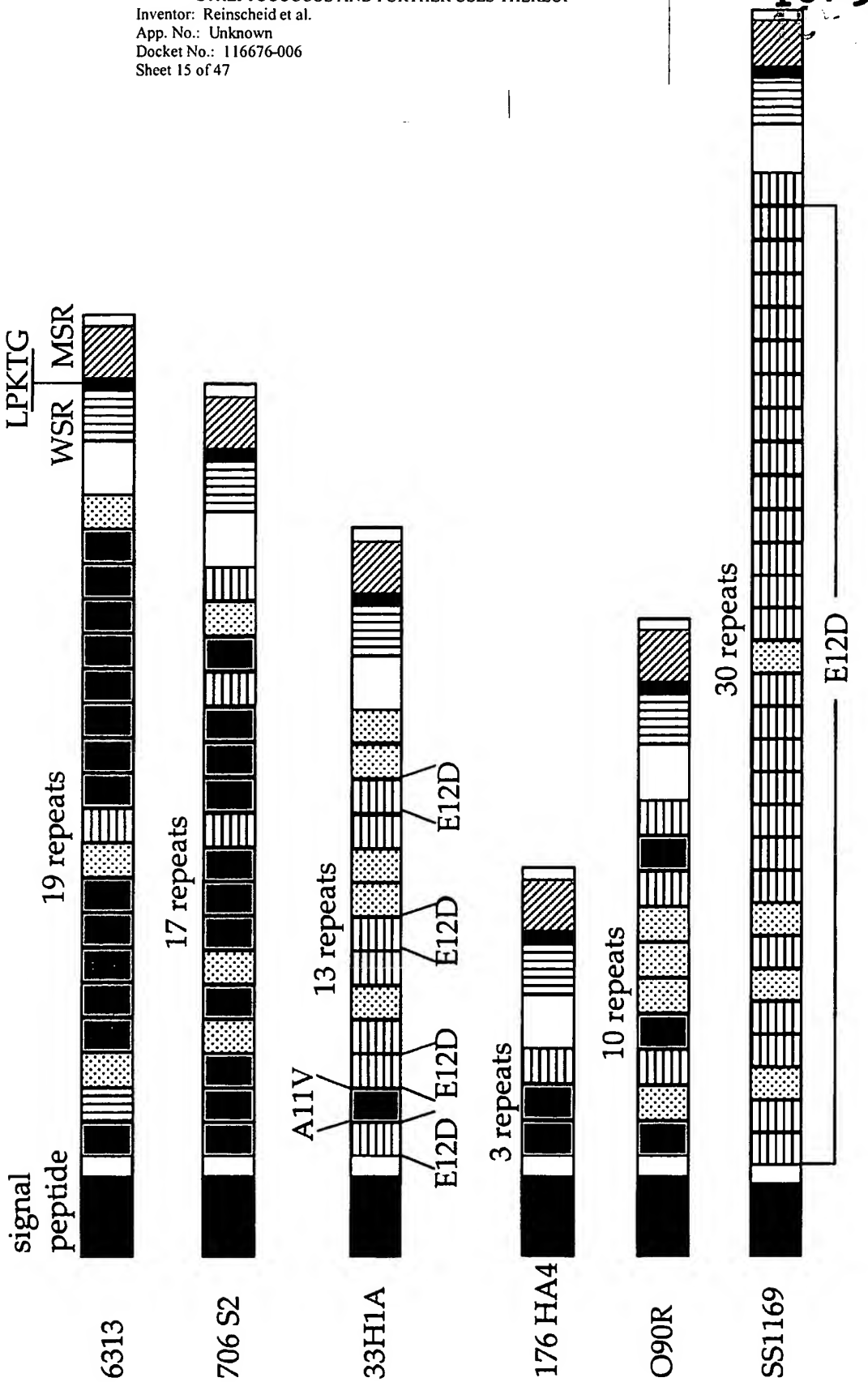

LPKTG
MSR
WSR
19 repeats
17 repeats
13 repeats
A11V
E12D
E12D
E12D
E12D
3 repeats
10 repeats
30 repeats
E12D
signal peptide
6313
706 S2
33H1A
176 HA4
O90R
SS1169

Fig. 8

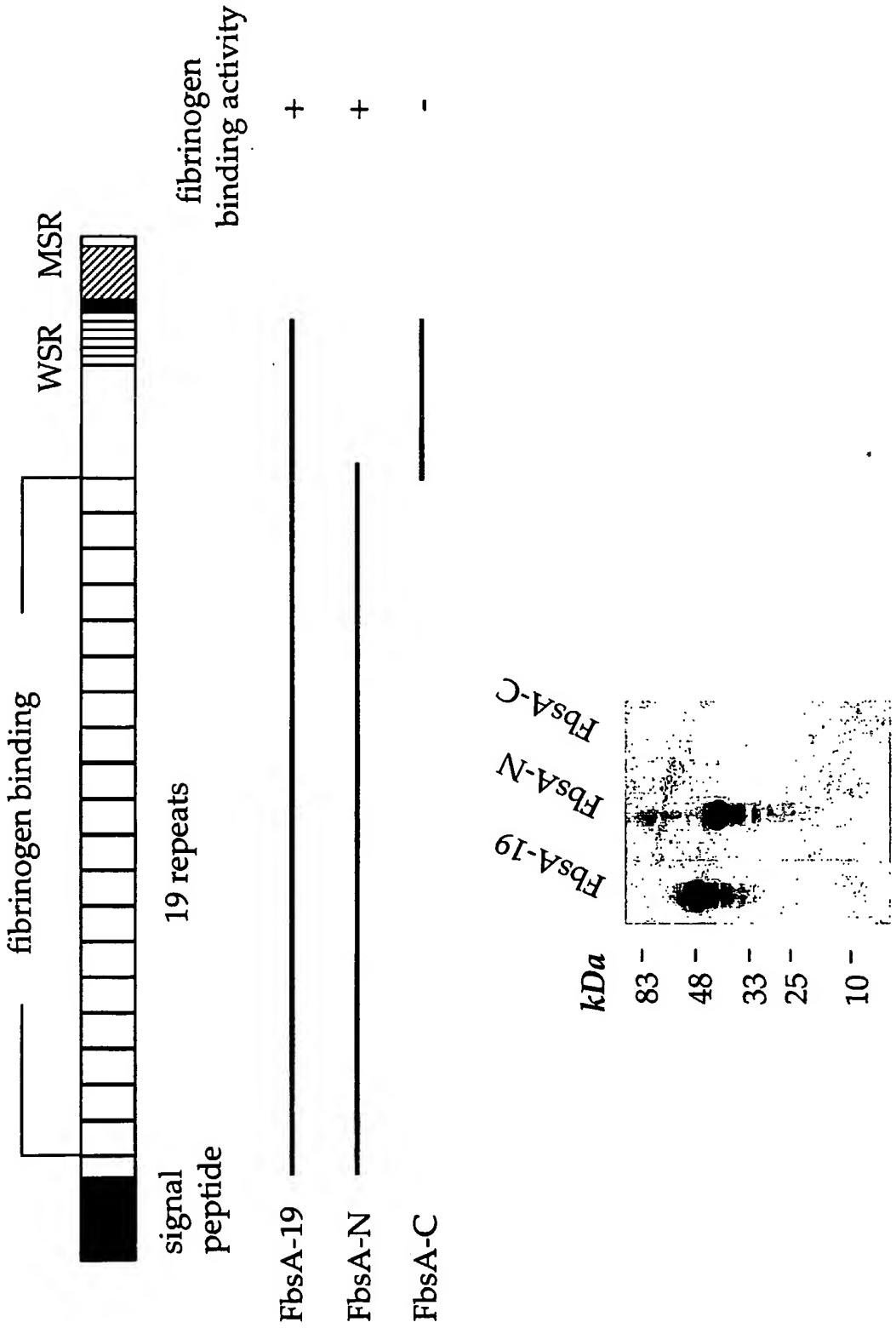

fibrinogen binding activity
+
+
-
MSR
WSR
fibrinogen binding
19 repeats
signal peptide
FbsA-19
FbsA-N
FbsA-C
FbsA-C
FbsA-N
FbsA-19
kDa
83
48
33
25
10

Fig. 9

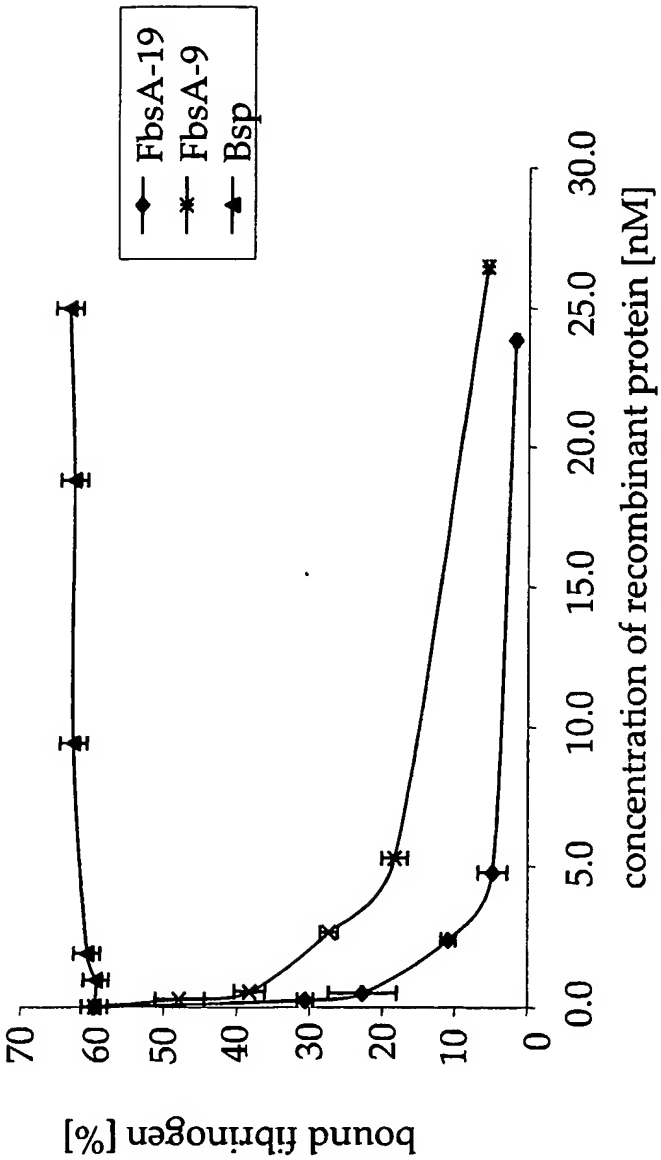

FbsA-19
FbsA-9
Bsp
concentration of recombinant protein [nM]
0.0
5.0
10.0
15.0
20.0
25.0
30.0
bound fibrinogen [%]
0
10
20
30
40
50
60
70

Fig. 10

GNVLERRQRDAENRSQ (SeqID 204)
G**LSQNRDVRENQRARE** (SeqID205)
GNVLERRQRDAENRSQ
G**LSQNRDVRENQRARE**
ANVLERRQRDAENRSQ (SeqID 206)
G**A**VLERRQRDAENRSQ (SeqID 207)
GN**A**LERRQRDAENRSQ (SeqID 208)
GNV**A**ERRQRDAENRSQ (SeqID 209)
GNVL**A**RRQRDAENRSQ (SeqID 210)
GNVLE**A**RQRDAENRSQ (SeqID 211)
GNVLER**A**QRDAENRSQ (SeqID 212)
GNVLERR**A**RDAENRSQ (SeqID 213)
GNVLERRQ**A**DAENRSQ (SeqID 214)
GNVLERRQR**A**AENRSQ (SeqID 215)
GNVLERRQRDAENRSQ (SeqID 216)
GNVLERRQRDA**A**NRSQ (SeqID 217)
GNVLERRQRDAE**A**RSQ (SeqID 218)
GNVLERRQRDAEN**A**SQ (SeqID 219)
GNVLERRQRDAENR**A**Q (SeqID 220)
GNVLERRQRDAENRS**A** (SeqID 221)
GNVLERRQRDAENRSQ
G**LSQNRDVRENQRARE**
GNVLERRQRDAENRSQ
G**LSQNRDVRENQRARE**

Fig. 11

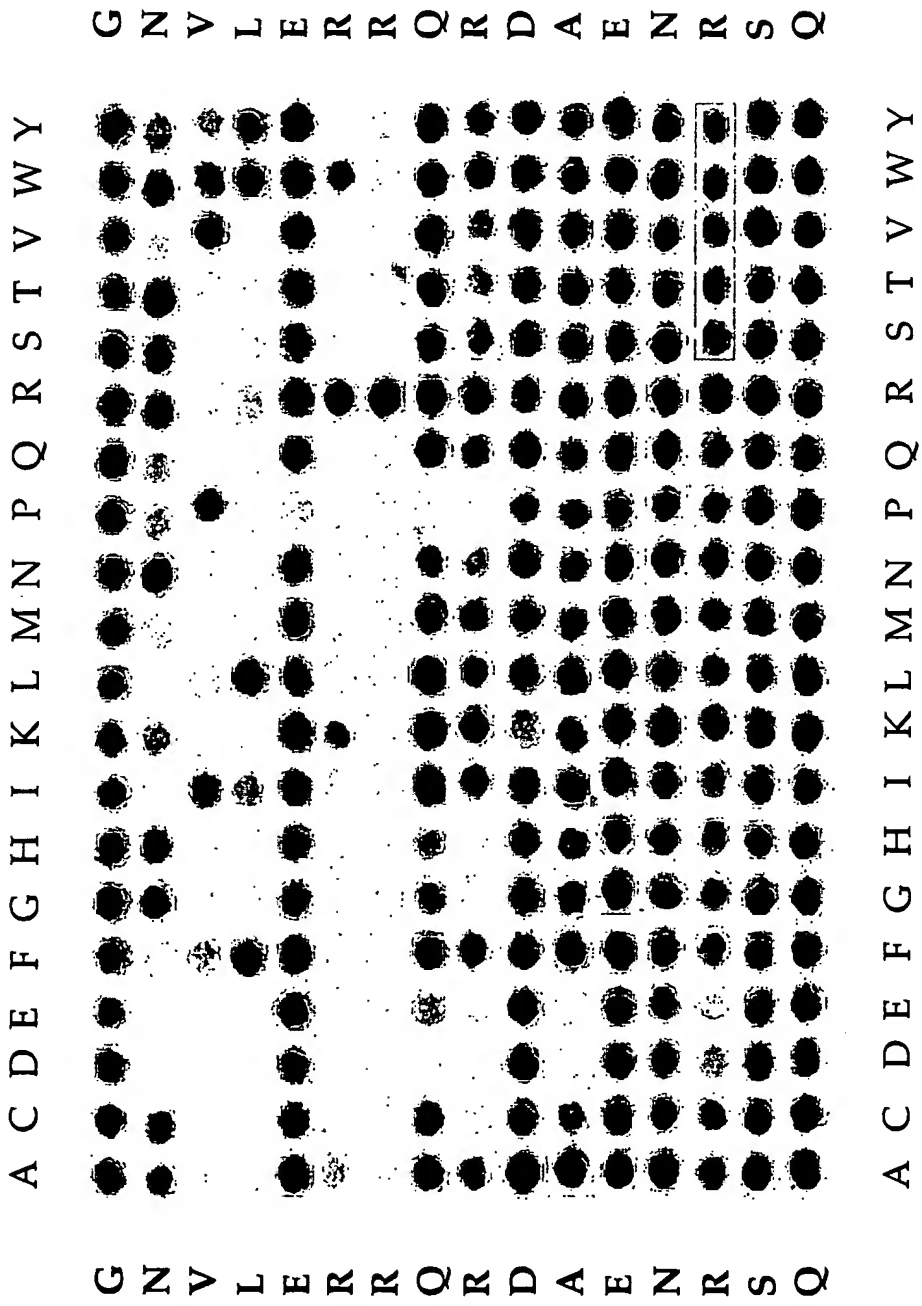

G N V L E R R Q R D A E N R S Q
A C D E F G H I K L M N P Q R S T V W Y
G N V L E R R Q R D A E N R S Q

Fig. 12

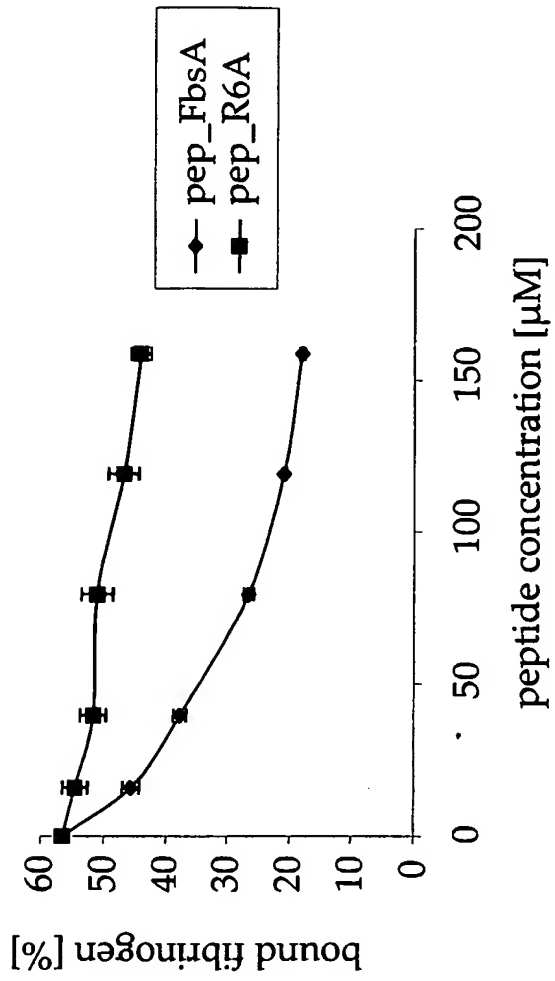

pep_FbsA
pep_R6A
bound fibrinogen [%]
60
50
40
30
20
10
0
0
50
100
150
200
peptide concentration [µM]

Fig. 13

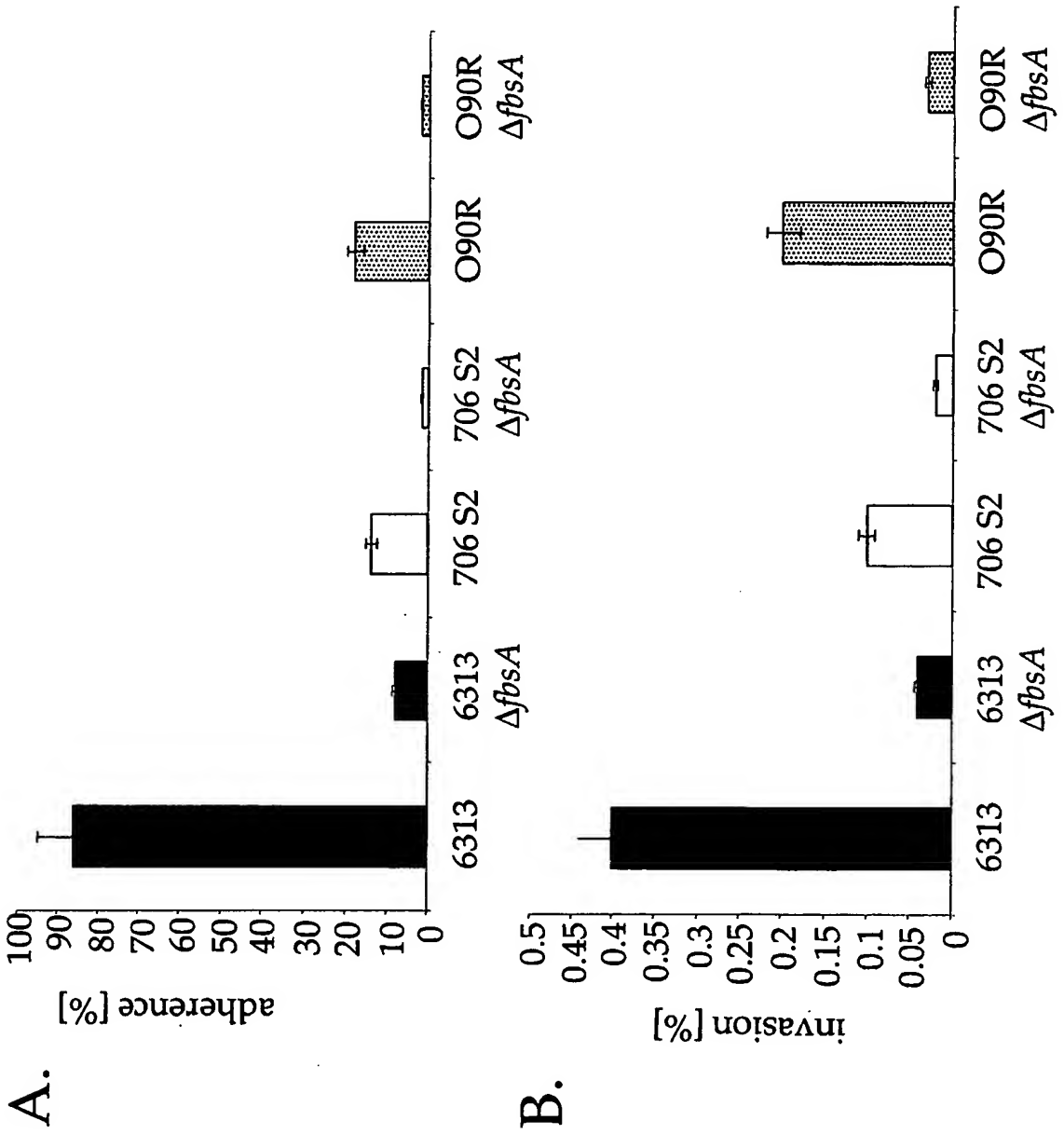

A.
adherence [%]
100
90
80
70
60
50
40
30
20
10
0
6313
6313 ΔfbsA
706 S2
706 S2 ΔfbsA
O90R
O90R ΔfbsA
B.
invasion [%]
0.5
0.45
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
6313
6313 ΔfbsA
706 S2
706 S2 ΔfbsA
O90R
O90R ΔfbsA

Fig. 14

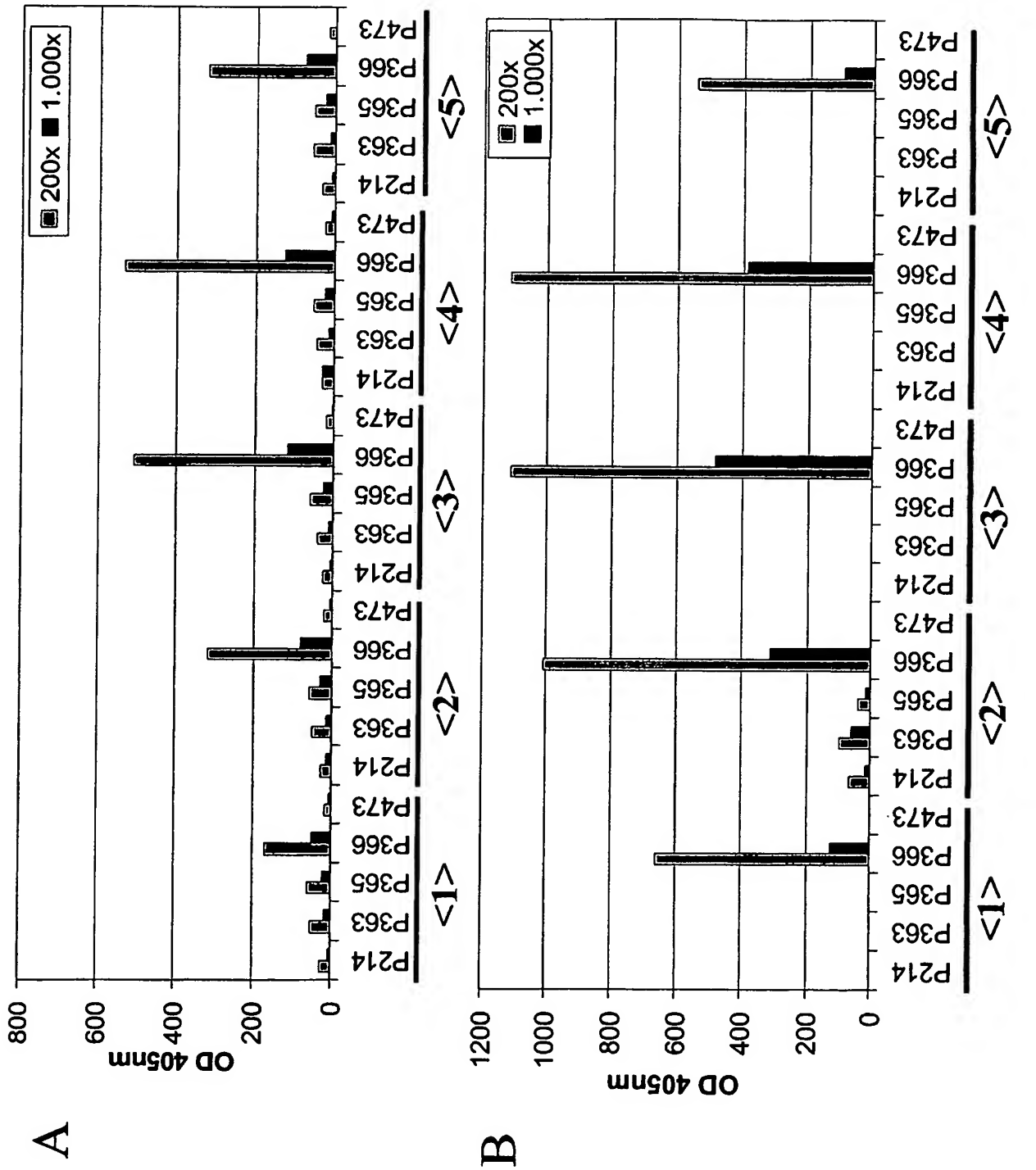

200x
1.000x
OD 405nm
0
200
400
600
800
1000
1200
P214
P363
P365
P366
P473
<1>
<2>
<3>
<4>
<5>
A
B

Fig. 15

1
ATTTTTAAGCAATATTTTAAAACATAAAAAAAGAAAAATCAACTACTTAAGCTAATTGAA
61
GTATTTCTAAGATAATAAAAAATAAGATTATCAAATAAAAAGAAAAATCATTCAAAAATT
121
GGGAAAAAACTTTAAAATTCCATACCTTATAATAAGAAATTATTGATATCATAATAAGTG
181
ATAGTTTGTATATTCTAGGATATTCTGTATCTGATCTTAGATTTAGAAACGACATTTCGG
241
CACAATAGGAGTTGTAAAATGAGAAAATACCAAAAATTTTCTAAAATATTGACGTTAAGT
301 RBS *M R K Y Q K F S K I L T L S*
CTTTTTTGTTTGTCGCAAATACCGCTTAATACCAATGTTTTAGGGGAAAGTACCGTACCG
L F C L S Q I P L N T N V L G E S T V P
361
GAAAATGGTGCTAAAGGAAAGTTAGTTGTTAAAAAGACAGATGACCAGAACAAACCACTT
E N G A K G K L V V K K T D D Q N K P L
421
TCAAAAGCTACCTTTGTTTTAAAAACTACTGCTCATCCAGAAAGTAAAATAGAAAAAGTA
S K A T F V L K T T A H P E S K I E K V
481
ACTGCTGAGCTAACAGGTGAAGCTACTTTTGATAATCTCATACCTGGAGATTATACTTTA
T A E L T G E A T F D N L I P G D Y T L
541
TCAGAAGAAACAGCGCCCGAAGGTTATAAAAAGACTAACCAGACTTGGCAAGTTAAGGTT
S E E T A P E G Y K K T N Q T W Q V K V
601
GAGAGTAATGGAAAAACTACGATACAAAATAGTGGTGATAAAAATTCCACAATTGGACAA
E S N G K T T I Q N S G D K N S T I G Q
661
AATCACGAAGAACTAGATAAGCAGTATCCCCCCACAGGAATTTATGAAGATACAAAGGAA
N H E E L D K Q Y P P T G I Y E D T K E
721
TCTTATAAACTTGAGCATGTTAAAGGTTCAGTTCCAAATGGAAAGTCAGAGGCAAAAGCA
S Y K L E H V K G S V P N G K S E A K A
781
GTTAACCCATATTCAAGTGAAGGTGAGCATATAAGAGAAATTCCAGAGGGAACATTATCT
V N P Y S S E G E H I R E I P E G T L S
841
AAACGTATTTCAGAAGTAGGTGATTTAGCTCATAATAAATATAAAATTGAGTTAACTGTC
K R I S E V G D L A H N K Y K I E L T V
901
AGTGGAAAAACCATAGTAAAACCAGTGGACAAACAAAAGCCGTTAGATGTTGTCTTCGTA
S G K T I V K P V D K Q K P L D V V F V
961
CTCGATAATTCTAACTCAATGAATAACGATGGCCCAAATTTTCAAAGGCATAATAAAGCC
L D N S N S M N N D G P N F Q R H N K A
1021

Fig. 16-1

```
AAGAAAGCTGCCGAAGCTCTTGGGACCGCAGTAAAAGATATTTTAGGAGCAAACAGTGAT
 K  K  A  A  E  A  L  G  T  A  V  K  D  I  L  G  A  N  S  D
1081
AATAGGGTTGCATTAGTTACCTATGGTTCAGATATTTTTGATGGTAGGAGTGTAGATGTC
 N  R  V  A  L  V  T  Y  G  S  D  I  F  D  G  R  S  V  D  V

1141
GTAAAAGGATTTAAAGAAGATGATAAATATTATGGCCTTCAAACTAAGTTCACAATTCAG
 V  K  G  F  K  E  D  D  K  Y  Y  G  L  Q  T  K  F  T  I  Q
1201
ACAGAGAATTATAGTCATAAACAATTAACAAATAATGCTGAAGAGATTATAAAAAGGATT
 T  E  N  Y  S  H  K  Q  L  T  N  N  A  E  E  I  I  K  R  I
1261
CCTACAGAAGCTCCTAGAGCTAAATGGGGATCAACTACAAACGGACTTACTCCAGAGCAA
 P  T  E  A  P  R  A  K  W  G  S  T  T  N  G  L  T  P  E  Q
1321
CAAAAGCAGTACTATCTTAGTAAAGTAGGGGAAACATTTACTATGAAAGCCTTCATGGAG
 Q  K  Q  Y  Y  L  S  K  V  G  E  T  F  T  M  K  A  F  M  E
1381
GCAGATGATATTTTGAGTCAAGTAGATCGAAATAGTCAAAAAATTATTGTTCATATAACT
 A  D  D  I  L  S  Q  V  D  R  N  S  Q  K  I  I  V  H  I  T
1441
GATGGTGTTCCAACAAGATCATATGCTATTAATAATTTTAAATTGGGTGCATCATATGAA
 D  G  V  P  T  R  S  Y  A  I  N  N  F  K  L  G  A  S  Y  E
1501
AGCCAATTTGAACAAATGAAAAAAAATGGATATCTAAATAAAAGTAATTTTCTACTTACT
 S  Q  F  E  Q  M  K  K  N  G  Y  L  N  K  S  N  F  L  L  T
1561
GATAAGCCCGAGGATATAAAAGGAAATGGGGAGAGTTACTTTTTGTTTCCCTTAGATAGT
 D  K  P  E  D  I  K  G  N  G  E  S  Y  F  L  F  P  L  D  S
1621
TATCAAACACAGATAATCTCTGGAAACTTACAAAAACTTCATTATTTAGATTTAAATCTT
 Y  Q  T  Q  I  I  S  G  N  L  Q  K  L  H  Y  L  D  L  N  L
1681
AATTACCCTAAAGGTACAATTTATCGAAATGGACCAGTAAGAGAACATGGAACACCAACC
 N  Y  P  K  G  T  I  Y  R  N  G  P  V  R  E  H  G  T  P  T
1741
AAACTTTATATAAATAGTTTAAAACAGAAAAATTATGACATCTTTAATTTTGGTATAGAT
 K  L  Y  I  N  S  L  K  Q  K  N  Y  D  I  F  N  F  G  I  D
1801
ATATCTGCTTTTAGACAAGTTTATAATGAGGATTATAAGAAAAATCAAGATGGTACTTTT
 I  S  A  F  R  Q  V  Y  N  E  D  Y  K  K  N  Q  D  G  T  F
1861
CAAAAATTGAAAGAGGAAGCTTTTGAACTTTCAGATGGGGAAATAACAGAACTAATGAAG
 Q  K  L  K  E  E  A  F  E  L  S  D  G  E  I  T  E  L  M  K
1921
TCATTCTCTTCTAAACCTGAGTATTATACCCCGATAGTAACTTCATCCGATGCATCTAAC
 S  F  S  S  K  P  E  Y  Y  T  P  I  V  T  S  S  D  A  S  N
1981
```

Fig. 16-2

```
AATGAAATTTTATCTAAAATTCAGCAACAATTTGAAAAGGTTTTAACAAAAGAAAACTCA
 N  E  I  L  S  K  I  Q  Q  Q  F  E  K  V  L  T  K  E  N  S
2041
ATTGTTAATGGAACTATAGAAGATCCTATGGGTGACAAAATCAATTTACAGCTTGGCAAC
 I  V  N  G  T  I  E  D  P  M  G  D  K  I  N  L  Q  L  G  N
2101
GGACAAACATTGCAACCAAGTGATTATACTTTACAGGGAAATGATGGAAGTATAATGAAA
 G  Q  T  L  Q  P  S  D  Y  T  L  Q  G  N  D  G  S  I  M  K
2161
GATAGCATTGCAACTGGTGGGCCTAATAATGATGGTGGAATACTTAAAGGGGTTAAATTA
 D  S  I  A  T  G  G  P  N  N  D  G  G  I  L  K  G  V  K  L
2221
GAATACATCAAAAATAAACTCTACGTTAGAGGTTTGAACTTAGGGGAGGGACAAAAAGTA
 E  Y  I  K  N  K  L  Y  V  R  G  L  N  L  G  E  G  Q  K  V
2281
ACACTCACATATGATGTGAAACTAGATGACAGTTTTATAAGTAACAAATTCTATGACACT
 T  L  T  Y  D  V  K  L  D  D  S  F  I  S  N  K  F  Y  D  T
2341
AATGGTAGAACAACATTGAATCCTAAATCAGAGGATCCTAATACACTTAGAGATTTTCCA
 N  G  R  T  T  L  N  P  K  S  E  D  P  N  T  L  R  D  F  P
2401
ATCCCTAAAATTCGTGATGTGAGAGAATATCCTACAATAACGATTAAAAACGAGAAGAAG
 I  P  K  I  R  D  V  R  E  Y  P  T  I  T  I  K  N  E  K  K
2461
TTAGGTGAAATTGAATTTACAAAAGTTGATAAAGATAATAATAAGTTGCTTCTCAAAGGA
 L  G  E  I  E  F  T  K  V  D  K  D  N  N  K  L  L  L  K  G
2521
GCTACGTTTGAACTTCAAGAATTTAATGAAGATTATAAACTTTATTTACCAATAAAAAAT
 A  T  F  E  L  Q  E  F  N  E  D  Y  K  L  Y  L  P  I  K  N
2581
AATAATTCAAAAGTAGTGACGGGAGAAAACGGCAAAATTTCTTACAAAGATTTGAAAGAT
 N  N  S  K  V  V  T  G  E  N  G  K  I  S  Y  K  D  L  K  D
2641
GGCAAATATCAGTTAATAGAAGCAGTTTCGCCGAAGGATTATCAAAAAATTACTAATAAA
 G  K  Y  Q  L  I  E  A  V  S  P  K  D  Y  Q  K  I  T  N  K
2701
CCAATTTTAACTTTTGAAGTTGTTAAAGGATCGATACAAAATATAATAGCTGTTAATAAA
 P  I  L  T  F  E  V  V  K  G  S  I  Q  N  I  I  A  V  N  K
2761
CAGATTTCTGAATATCATGAGGAAGGTGACAAGCATTTAATTACCAACACGCATATTCCA
 Q  I  S  E  Y  H  E  E  G  D  K  H  L  I  T  N  T  H  I  P
2821
CCAAAAGGAATTATTCCGATGACAGGTGGGAAAGGAATTCTATCTTTCATTTTAATAGGT
 P  K  G  I  I  P  M  T  G  G  K  G  I  L  S  F  I  L  I  G
2881
GGATCTATGATGTCTATTGCAGGTGGAATTTATATTTGGAAAAGATATAAGAAATCTAGT
 G  S  M  M  S  I  A  G  G  I  Y  I  W  K  R  Y  K  K  S  S
2941
```

Fig. 16-3

```
GATATATCTAGAGAAAAAGATTAAGAATCATGTGTTTTAGTATTCTTAATTAATTAAATA
 D  I  S  R  E  K  D  *
3001
TAATTCGAAAGGAGTGGTGCTGCGGTAATATTATAATCCGTATATTATTATCTATGTTGA
3061
TTAACTAGAATAAGAAGGAGATAGAAATGAAAAAAATCAACAAATGTCTTACAGTGTTCT
3121              RBS          M  K  K  I  N  K  C  L  T  V  F
CGACACTGCTATTGATCTTAACGTCACTATTCTCAGTTGCACCAGCGTTTGCGGACGACG
S  T  L  L  L  I  L  T  S  L  F  S  V  A  P  A  F  A  D  D
3181
TAACAACTGATACTGTGACCTTGCACAAGATTGTCATGCCACAAGCTGCATTTGATAACT
V  T  T  D  T  V  T  L  H  K  I  V  M  P  Q  A  A  F  D  N
3241
TTACTGAAGGTACAAAAGGTAAGAATGATAGCGATTATGTTGGTAAACAAATTAATGACC
F  T  E  G  T  K  G  K  N  D  S  D  Y  V  G  K  Q  I  N  D
3301
TTAAATCTTATTTTGGCTCAACCGATGCTAAAGAAATTAAGGGTGCTTTCTTTGTTTTCA
L  K  S  Y  F  G  S  T  D  A  K  E  I  K  G  A  F  F  V  F
3361
AAAATGAAACTGGTACAAAATTCATTACTGAAAATGGTAAGGAAGTCGATACTTTGGAAG
K  N  E  T  G  T  K  F  I  T  E  N  G  K  E  V  D  T  L  E
3421
CTAAAGATGCTGAAGGTGGTGCTGTTCTTTCAGGGTTAACAAAAGACACTGGTTTTGCTT
A  K  D  A  E  G  G  A  V  L  S  G  L  T  K  D  T  G  F  A
3481
TTAACACTGCTAAGTTAAAAGGAACTTACCAAATCGTTGAATTGAAAGAAAAATCAAACT
F  N  T  A  K  L  K  G  T  Y  Q  I  V  E  L  K  E  K  S  N
3541
ACGATAACAACGGTTCTATCTTGGCTGATTCAAAAGCAGTTCCAGTTAAAATCACTCTGC
Y  D  N  N  G  S  I  L  A  D  S  K  A  V  P  V  K  I  T  L
3601
CATTGGTAAACAACCAAGGTGTTGTTAAAGATGCTCACATTTATCCAAAGAATACTGAAA
P  L  V  N  N  Q  G  V  V  K  D  A  H  I  Y  P  K  N  T  E
3661
CAAAACCACAAGTAGATAAGAACTTTGCAGATAAAGATCTTGATTATACTGACAACCGAA
T  K  P  Q  V  D  K  N  F  A  D  K  D  L  D  Y  T  D  N  R
3721
AAGACAAAGGTGTTGTCTCAGCGACAGTTGGTGACAAAAAAGAATACATAGTTGGAACAA
K  D  K  G  V  V  S  A  T  V  G  D  K  K  E  Y  I  V  G  T
3781
AAATTCTTAAAGGCTCAGACTATAAGAAACTGGTTTGGACTGATAGCATGACTAAAGGTT
K  I  L  K  G  S  D  Y  K  K  L  V  W  T  D  S  M  T  K  G
3841
TGACGTTCAACAACAACGTTAAAGTAACATTGGATGGTAAAGATTTTCCTGTTTTAAACT
L  T  F  N  N  N  V  K  V  T  L  D  G  K  D  F  P  V  L  N
3901
ACAAACTCGTAACAGATGACCAAGGTTTCCGTCTTGCCTTGAATGCAACAGGTCTTGCAG
Y  K  L  V  T  D  D  Q  G  F  R  L  A  L  N  A  T  G  L  A
3961
```

Fig. 16-4

```
CAGTAGCAGCTGCTGCAAAAGACAAAGATGTTGAAATCAAGATCACTTACTCAGCTACGG
A  V  A  A  A  A  K  D  K  D  V  E  I  K  I  T  Y  S  A  T
4021
TGAACGGCTCCACTACTGTTGAAGTTCCAGAAACCAATGATGTTAAATTGGACTATGGTA
V  N  G  S  T  T  V  E  V  P  E  T  N  D  V  K  L  D  Y  G
4081
ATAACCCAACGGAAGAAAGTGAACCACAAGAAGGTACTCCAGCTAACCAAGAAATTAAAG
N  N  P  T  E  E  S  E  P  Q  E  G  T  P  A  N  Q  E  I  K
4141
TCATTAAAGACTGGGCAGTAGATGGTACAATTACTGATGTTAATGTTGCAGTTAAAGCTA
V  I  K  D  W  A  V  D  G  T  I  T  D  V  N  V  A  V  K  A
4201
TCTTTACCTTGCAAGAAAAACAAACGGATGGTACATGGGTGAACGTTGCTTCACACGAAG
I  F  T  L  Q  E  K  Q  T  D  G  T  W  V  N  V  A  S  H  E
4261
CAACAAAACCATCACGCTTTGAACATACTTTCACAGGTTTGGATAATACTAAAACTTACC
A  T  K  P  S  R  F  E  H  T  F  T  G  L  D  N  T  K  T  Y
4321
GCGTTGTCGAACGTGTTAGCGGCTACACTCCAGAATATGTATCATTTAAAAATGGTGTTG
R  V  V  E  R  V  S  G  Y  T  P  E  Y  V  S  F  K  N  G  V
4381
TGACTATCAAGAACAACAAAAACTCAAATGATCCAACTCCAATCAACCCATCAGAACCAA
V  T  I  K  N  N  K  N  S  N  D  P  T  P  I  N  P  S  E  P
4441
AAGTGGTGACTTATGGACGTAAATTTGTGAAAACAAATCAAGCTAACACTGAACGCTTGG
K  V  V  T  Y  G  R  K  F  V  K  T  N  Q  A  N  T  E  R  L
4501
CAGGAGCTACCTTCCTTGTTAAGAAAGAAGGAAAATACTTGGCACGTAAAGCAGGTGCAG
A  G  A  T  F  L  V  K  K  E  G  K  Y  L  A  R  K  A  G  A
4561
CAACTGCTGAAGCAAAGGCAGCTGTAAAAACTGCTAAACTAGCATTGGATGAAGCTGTTA
A  T  A  E  A  K  A  A  V  K  T  A  K  L  A  L  D  E  A  V
4621
AAGCTTATAACGACTTGACTAAAGAAAAACAAGAAGGCCAAGAAGGTAAAACAGCATTGG
K  A  Y  N  D  L  T  K  E  K  Q  E  G  Q  E  G  K  T  A  L
4681
CTACTGTTGATCAAAAACAAAAAGCTTACAATGACGCTTTTGTTAAAGCTAACTACTCAT
A  T  V  D  Q  K  Q  K  A  Y  N  D  A  F  V  K  A  N  Y  S
4741
ATGAATGGGTTGCAGATAAAAAGGCTGATAATGTTGTTAAATTGATCTCTAACGCCGGTG
Y  E  W  V  A  D  K  K  A  D  N  V  V  K  L  I  S  N  A  G
4801
GTCAATTTGAAATTACTGGTTTGGATAAAGGCACTTATAGCTTGGAAGAAACTCAAGCAC
G  Q  F  E  I  T  G  L  D  K  G  T  Y  S  L  E  E  T  Q  A
4861
CAGCAGGTTATGCGACATTGTCAGGTGATGTAAACTTTGAAGTAACTGCCACATCATATA
P  A  G  Y  A  T  L  S  G  D  V  N  F  E  V  T  A  T  S  Y
4921
```

Fig. 16-5

GCAAAGGGGCTACAACTGACATCGCATATGATAAAGGATCTGTAAAAAAAGATGCCCAAC
S K G A T T D I A Y D K G S V K K D A Q
4981
AAGTTCAAAACAAAAAAGTAACCATCCCACAAACAGGTGGTATTGGTACAATTCTTTTCA
Q V Q N K K V T **I P Q T G** G I G T I L F
5041
CAATTATTGGTTTAAGCATTATGCTTGGAGCAGTAGTTGTCATGAAAAAACGTCAATCAG
T I I G L S I M L G A V V V M K K R Q S
5101
AGGAAGCTTAAGGCTAGTCTTTGATGGTGTATAAGCACAGTTAAAGCTGTGCTTATGATC
E E A *
5161
TAAGGGTATTTCAGTAGAAGTACTCTTAGATCATAAGCAAGAGCCATTATTTAGGAGATG
5221
ACGTGAAGACTAAAAATATCAACAAAAAAACTAAAAAGAAGAAGTCAAATCTTCCTTTTA
5281
TCATTCTTTTTCTAATAGGTCTATCTATTTTATTGTATCCAGTGGTATCACGTTTTTACT
5341
ATACGATAGAATCTAATAATCAAACACAGGATTTTGAGAGAG

Fig. 16-6

1
GCTCATGATAATTTATAGAACATTTATAAAATCTTATAATAAACTGGTTAAGTATAGGAA
61
ATACTGCATATTTCTTGAAAATATGGTGTATATTGTGAATAAAATGATGACCAAGTTAAT
121
TGAATTTTCCTATCGAAAAATTTTTCAAAAAAAATAATTTCACGCTCAAATCATTTGATT
181
GTCAAATAAATAGAGCCTTTATAAAAATATTATATAAGTATAAAATGTAAAAAAATAAAA
241
AAATGATATTTTTATTTGATTCAAATGTATTTAATAAAAATACAAAGTTTCTAAAAAAGT
301
AAAAATTCCATCTCAATAAACAGCGTTAGTTATTATAACCGAACATTATTGTCCTTAAAA
361
CATTAAAACAAAAACAAAAGTTCGTAATTTAATTAATTTGTCATGTTACTAATCTTATGC
421
TAATATATTATCTCGTGATAAGTTTTTGATGTAAAAATTATCATGAAAAAGAAAAGAGAG
481 RBS
ATGGAAATGAAAAAACAATTTTTAAAATCAGCAGCGATTCTATCGCTAGCAGTAACAGCA
541 ***M K K Q F L K S A A I L S L A V T A***
GTATCTACAAGTCAGCCGGTAGCCGGGATAACTAAAGATTATAATAACCGAAATGAAAAA
V S T S Q P V A G I T K D Y N N R N E K
601
GTAAAAAAGTATTTACAAGAAAATAATTTCGGTCATAAAATAGCGTATGGATGGAAAAAT
V K K Y L Q E N N F G H K I A Y G W K N
661
AAAGTAGAATTTGATTTTCGTTATTTATTGGATACTGCTAAATATTTAGTAAATAAAGAA
K V E F D F R Y L L D T A K Y L V N K E
721
GAATTTCAAGATCCTTTATATAATGATGCGCGCGAAGAATTGATAAGTTTTATTTTTCCT
E F Q D P L Y N D A R E E L I S F I F P
781
TATGAGAAATTTTTAATTAACAATCGTGACATAACTAAATTAACAGTTAATCAGTATGAA
Y E K F L I N N R D I T K L T V N Q Y E
841
GCGATTGTGAATAGAATGAGTGTTGCTTTACAAAAATTTTCAAAGAATATTTTTGAGAAA
A I V N R M S V A L Q K F S K N I F E K
901
CAGAAAGTAAATAAAGATTTAATCCCTATTGCGTTTTGGATTGAGAAAAGTTACAGAACT
Q K V N K D L I P I A F W I E K S Y R T
961
GTTGGAACGAATGAAATCGCCGCTTCTGTAGGCATTCAAGGAGGATTTTATCAAAACTTC
V G T N E I A A S V G I Q G G F Y Q N F
1021
CATGATTATTATAATTATTCATATCTATTAAATTCTTTATGGCATGAAGGAAATGTAAAA
H D Y Y N Y S Y L L N S L W H E G N V K
1081
GAAGTAGTTAAGGATTATGAAAACACTATTCGTCAAATACTATCTAAAAAGCATGAGATT
E V V K D Y E N T I R Q I L S K K H E I
1141

Fig. 17-1

```
GAAAAAATTCTTAATCAGAGCACTTCTGATATCTCTATAGATGATGATGATTACGAAAAA
 E  K  I  L  N  Q  S  T  S  D  I  S  I  D  D  D  D  Y  E  K
1201
GGAAATAAAGAATTGCTAAGGGAAAAATTAAATATTATTCTAAATCTTTCAAAGAGAGAT
 G  N  K  E  L  L  R  E  K  L  N  I  I  L  N  L  S  K  R  D
1261
TACAGAGTAACTCCATACTATGAAGTGAATAAACTACATACAGGGCTTATTTTATTGGAG
 Y  R  V  T  P  Y  Y  E  V  N  K  L  H  T  G  L  I  L  L  E
1321
GATGTCCCTAATTTAAAGATTGCTAAGGATAAGTTGTTCTCATTAGAGAATTCTTTAAAG
 D  V  P  N  L  K  I  A  K  D  K  L  F  S  L  E  N  S  L  K
1381
GAATACAAAGGAGAGAAAGTTAATTATGAGGAACTAAGATTCAATACGGAACCTTTAACT
 E  Y  K  G  E  K  V  N  Y  E  E  L  R  F  N  T  E  P  L  T
1441
AGTTACTTAGAAAATAAAGAAAAATTTTTAGTCCCCAATATTCCATATAAAAATAAATTA
 S  Y  L  E  N  K  E  K  F  L  V  P  N  I  P  Y  K  N  K  L
1501
ATTTTAAGGGAAGAAGATAAATATAGTTTTGAAGATGATGAAGAAGAGTTTGGAAATGAA
 I  L  R  E  E  D  K  Y  S  F  E  D  D  E  E  E  F  G  N  E
1561
CTTCTAAGTTACAATAAGCTTAAGAATGAAGTTTTACCTGTTAATATTACAACTTCTACT
 L  L  S  Y  N  K  L  K  N  E  V  L  P  V  N  I  T  T  S  T
1621
ATATTAAAACCGTTTGAACAGAAGAAAATTGTGGAAGATTTTAATCCTTATTCTAATTTA
 I  L  K  P  F  E  Q  K  K  I  V  E  D  F  N  P  Y  S  N  L
1681
GACAATTTAGAAATAAAAAAAATAAGGTTGAATGGCTCCCAAAAACAAAAAGTAGAACAG
 D  N  L  E  I  K  K  I  R  L  N  G  S  Q  K  Q  K  V  E  Q
1741
GAAAAAACTAAATCGCCAACTCCTCAAAAAGAGACTGTGAAAGAACAAACTGAGCAAAAA
 E  K  T  K  S  P  T  P  Q  K  E  T  V  K  E  Q  T  E  Q  K
1801
GTATCTGGAAATACTCAAGAGGTAGAAAAGAAATCTGAAACTGTGGCAACTTCACAACAA
 V  S  G  N  T  Q  E  V  E  K  K  S  E  T  V  A  T  S  Q  Q
1861
AGTTCAGTTGCGCAAACTTCTGTCCAACAGCCGGCTCCGGTTCAATCAGTTGTTCAAGAA
 S  S  V  A  Q  T  S  V  Q  Q  P  A  P  V  Q  S  V  V  Q  E
1921
TCCAAAGCTTCTCAAGAGGAGATTAATGCAGCACACGATGCTATTTCGGCGTATAAATCA
 S  K  A  S  Q  E  E  I  N  A  A  H  D  A  I  S  A  Y  K  S
1981
ACAGTCAATATTGCTAATACAGCCGGTGTAACAACTGCGGAAATGACCACGCTCATTAAT
 T  V  N  I  A  N  T  A  G  V  T  T  A  E  M  T  T  L  I  N
2041
ACTCAAACTTCTAATCTTTCTGATGTTGAGAAAGCTTTAGGAAATAATAAGGTTAATAAT
 T  Q  T  S  N  L  S  D  V  E  K  A  L  G  N  N  K  V  N  N
2101
GGTGCAGTCAATGTATTGAGAGAAGATACAGCTCGTCTTGAGAATATGATTTGGAATCGT
 G  A  V  N  V  L  R  E  D  T  A  R  L  E  N  M  I  W  N  R
2161
```

Fig. 17-2

```
GCTTACCAAGCTATTGAAGAATTCAACGTCGCTCGTAATACTTATAATAACCAAATCAAG
 A  Y  Q  A  I  E  E  F  N  V  A  R  N  T  Y  N  N  Q  I  K
2221
ACAGAAACAGTTCCAGTTGATAATGATATTGAAGCTATTTTAGCAGGTTCTCAAGCTAAA
 T  E  T  V  P  V  D  N  D  I  E  A  I  L  A  G  S  Q  A  K
2281
ATTAGCCATTTGGACAATCGTATCGGAGCGCGCCACATGGATCAAGCTTTTGTAGCTAGT
 I  S  H  L  D  N  R  I  G  A  R  H  M  D  Q  A  F  V  A  S
2341
TTATTAGAAGTTACTGAGATGAGTAAATCAATCTCATCGCGTATAAAAGAGTAGACACTG
 L  L  E  V  T  E  M  S  K  S  I  S  S  R  I  K  E  *
2401
CTATCAAGGCGATCTTAAACTTTTGTATTAAACTAACCTAAAAGATAGAAAGAGACTAAT
2461                                                  RBS
ATGAAAAAAATAACAACTTTAATCTTAGCTAGTAGCTTATTACTAGTTGCAACGACATCG
 M  K  K  I  T  T  L  I  L  A  S  S  L  L  L  V  A  T  T  S
2521
GTTAAAGCTGATGATAACTTTGAAATGCCAACGCGTTATGTTAAAATGAGTGAAAAATCA
 V  K  A  D  D  N  F  E  M  P  T  R  Y  V  K  M  S  E  K  S
2581
AAAGCATTTTATCAAAGACTACAAGAAAAACAACGTAAGGCACATACTACTGTGAAGACT
 K  A  F  Y  Q  R  L  Q  E  K  Q  R  K  A  H  T  T  V  K  T
2641
TTTAATAATTCAGAAATAAGGCATCAACTACCTCTTAAACAAGAAAAGGCTAGAAATGAT
 F  N  N  S  E  I  R  H  Q  L  P  L  K  Q  E  K  A  R  N  D
2701
ATCTACAATTTAGGCATTCTTATTTCTCAGGAGTCTAAAGGGTTCATCCAACGTATTGAT
 I  Y  N  L  G  I  L  I  S  Q  E  S  K  G  F  I  Q  R  I  D
2761
AATGCCTATTCTTTGGAAAATGTCTCAGATATTGTTAATGAAGCTCAGGCTTTGTATAAA
 N  A  Y  S  L  E  N  V  S  D  I  V  N  E  A  Q  A  L  Y  K
2821
CGTAACTATGATTTATTTGAAAAAATCAAATCTACACGTGATAAGGTTCAAGTCTTACTT
 R  N  Y  D  L  F  E  K  I  K  S  T  R  D  K  V  Q  V  L  L
2881
GCATCGCATCAAGATAATACAGACTTAAAAAACTTTTATGCTGAGTTAGATGATATGTAT
 A  S  H  Q  D  N  T  D  L  K  N  F  Y  A  E  L  D  D  M  Y
2941
GAACATGTTTATCTCAATGAAAGTAGAGTGGAGGCGATAAACAGAAATATCCAAAAATAT
 E  H  V  Y  L  N  E  S  R  V  E  A  I  N  R  N  I  Q  K  Y
3001
AATTAGTTTCTAAACTAACAAACATTCCTAAATATAAGATATTAAACCCTACTTATTGAT
 N  *
3061
TAGTGAGTAGGGTTTTACTGTTTTAAATAGCTTTCTGCTCAGAATGTAAGCCTTGTCATT
3121
TCAAAGGAACTATGTTATTATTCTTAAGTAAATTAAATAGGACATTTGGGGTGCGTAACA
3181
GCTGAGATTATACCCATTGA
```

Fig. 17-3

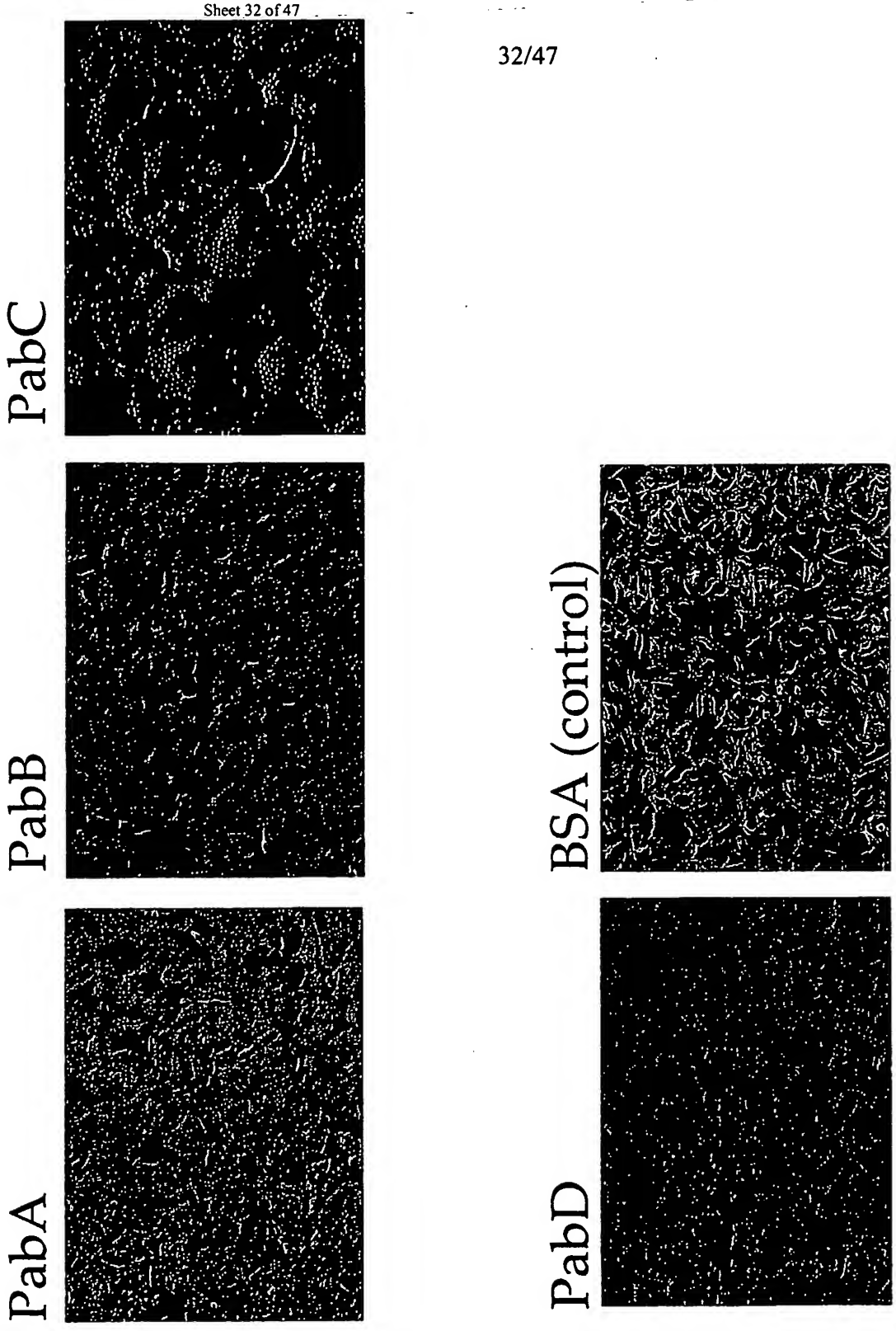
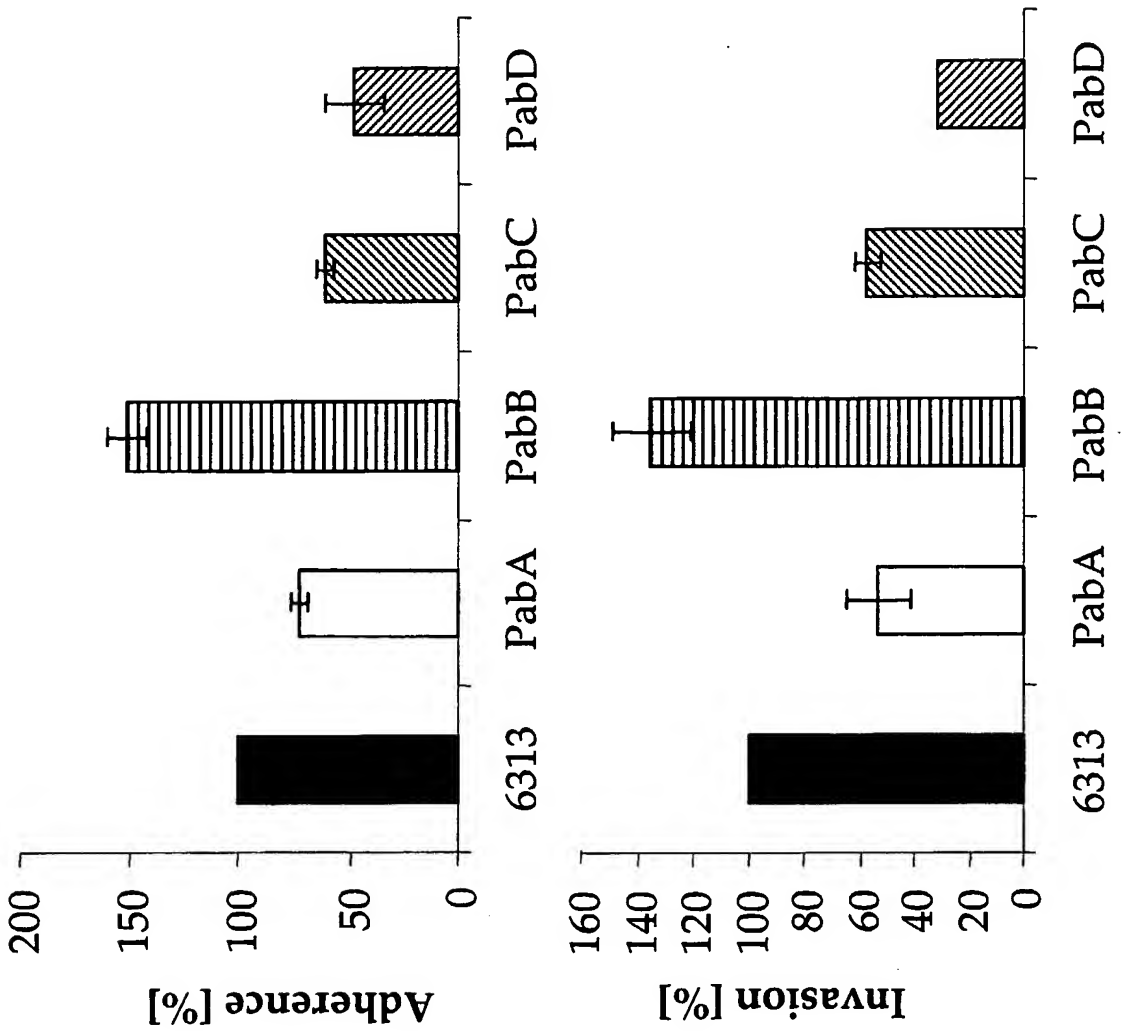


Fig. 18



A. Adherence of GBS 6313 in the presence of 100 µg/ml of different fusion proteins

B. Invasion of GBS 6313 in the presence of 100µg/ml of different fusion proteins

Fig. 19


B.
invasion [%]
100
80
60
40
20
0
6313
6313 ΔsapA
6313 ΔsapB
A.
adherence [%]
100
80
60
40
20
0
6313
6313 ΔsapA
6313 ΔsapB

Fig. 20

Fig. 21

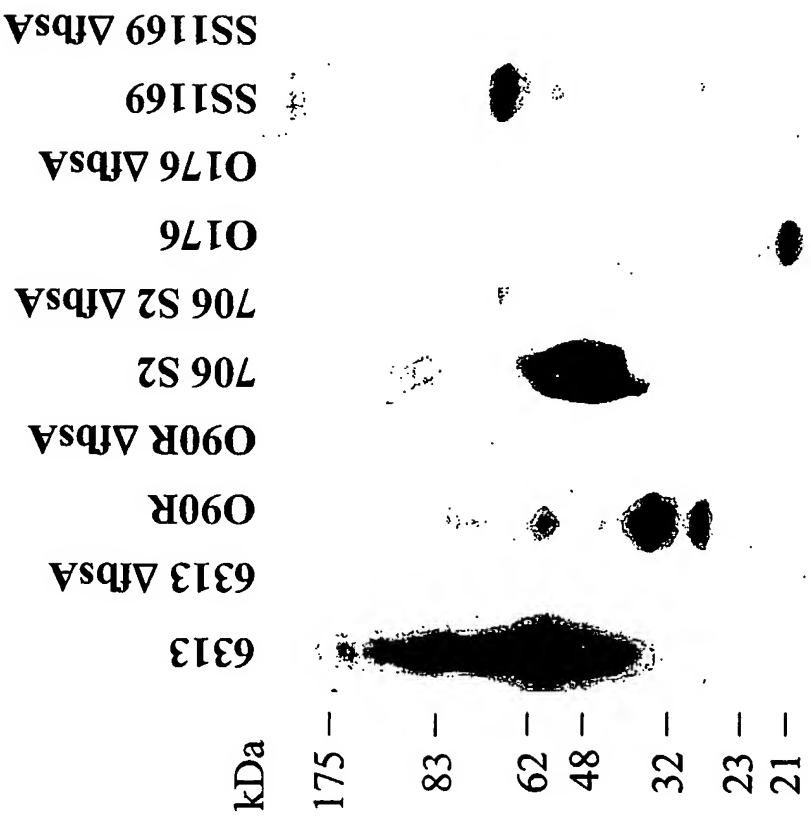

kDa
175
83
62
48
32
23
21
6313
6313 ΔfbsA
O90R
O90R ΔfbsA
706 S2
706 S2 ΔfbsA
O176
O176 ΔfbsA
SSI169
SSI169 ΔfbsA

Fig. 22

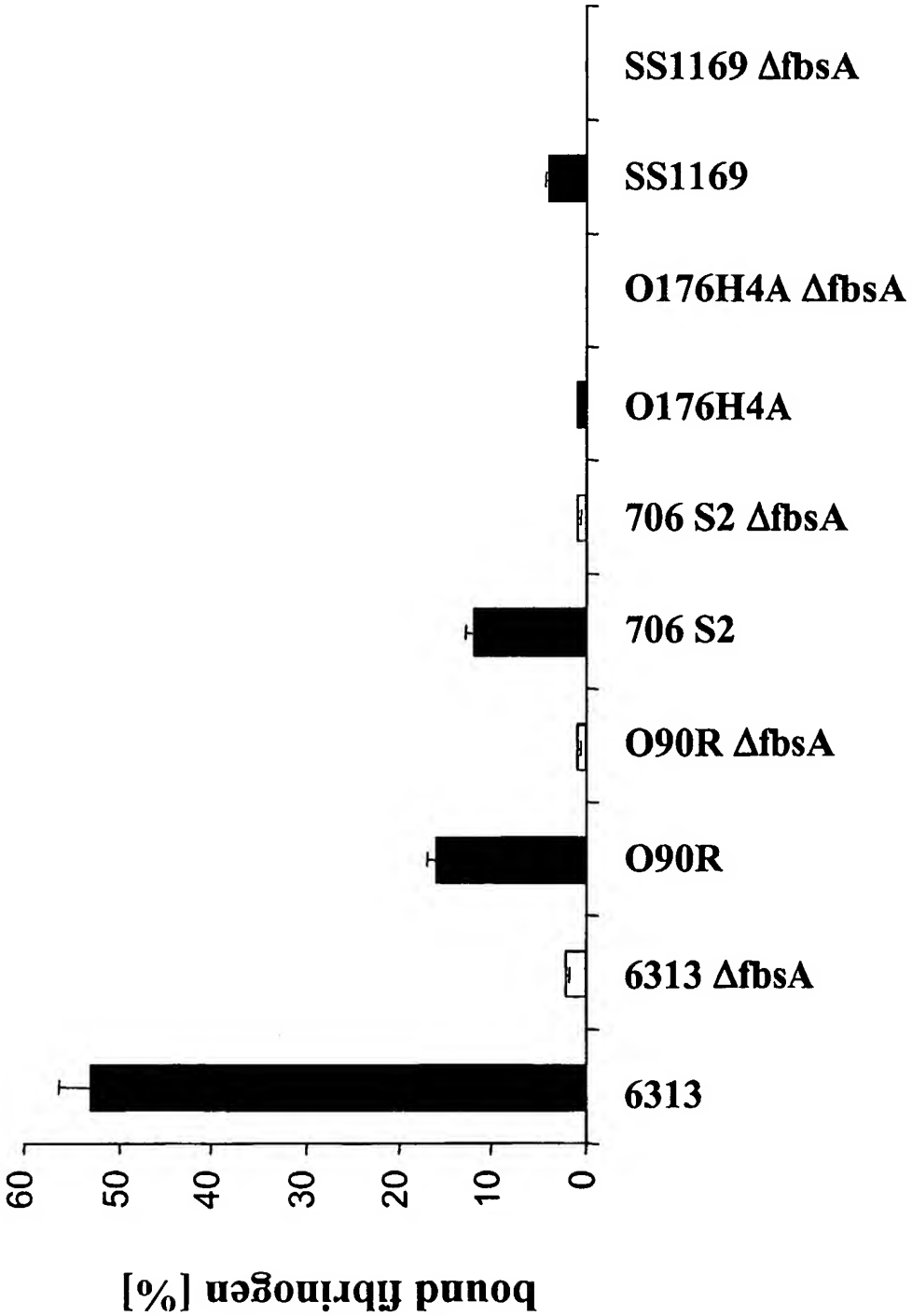

SS1169 ΔfbsA
SS1169
O176H4A ΔfbsA
O176H4A
706 S2 ΔfbsA
706 S2
O90R ΔfbsA
O90R
6313 ΔfbsA
6313
60
50
40
30
20
10
0
bound fibrinogen [%]

Fig. 23

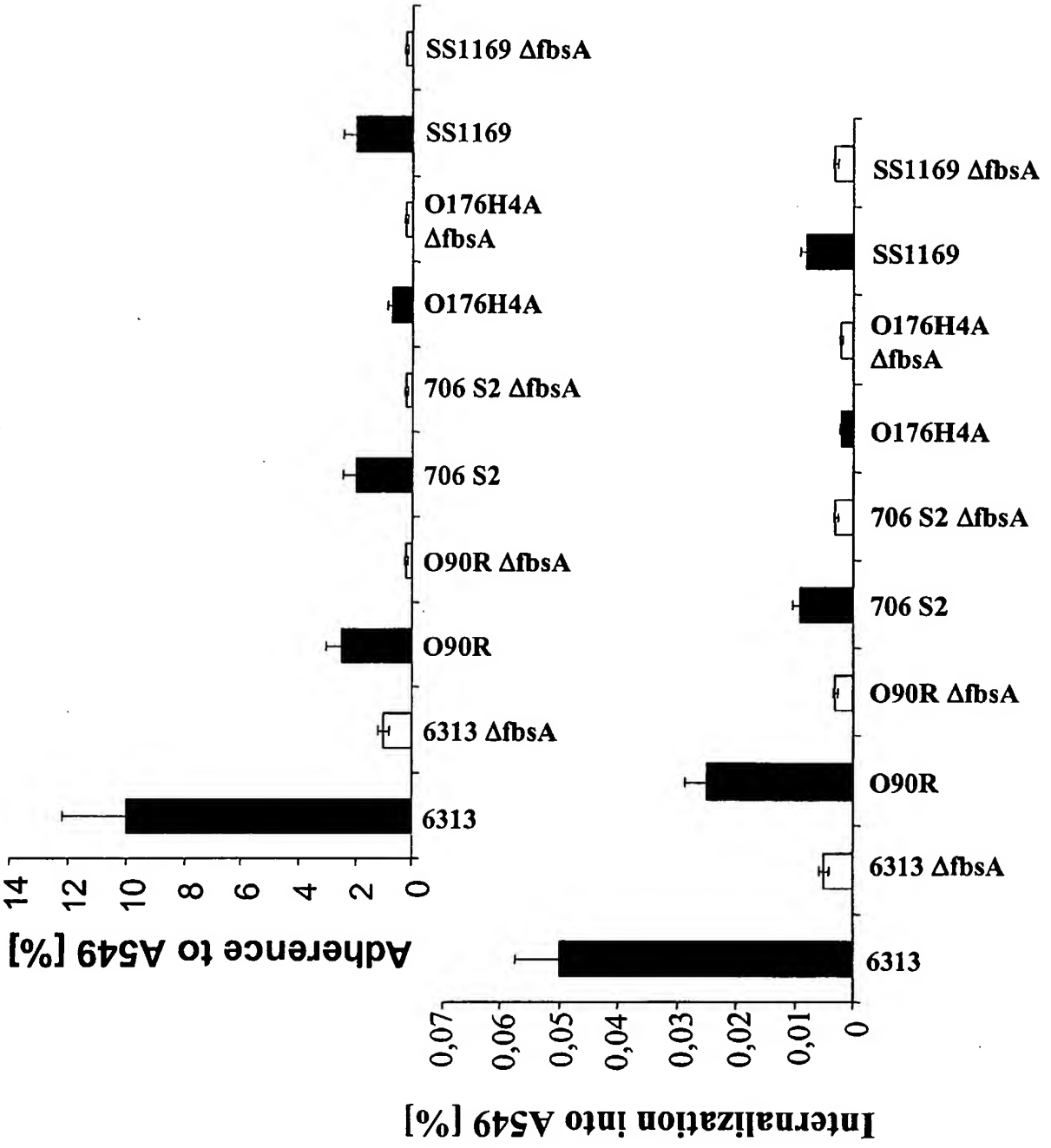

SS1169 ΔfbsA
SS1169
O176H4A ΔfbsA
O176H4A
706 S2 ΔfbsA
706 S2
O90R ΔfbsA
O90R
6313 ΔfbsA
6313
14
12
10
8
6
4
2
0
Adherence to A549 [%]
SS1169 ΔfbsA
SS1169
O176H4A ΔfbsA
O176H4A
706 S2 ΔfbsA
706 S2
O90R ΔfbsA
O90R
6313 ΔfbsA
6313
0,07
0,06
0,05
0,04
0,03
0,02
0,01
0
Internalization into A549 [%]

Fig. 24

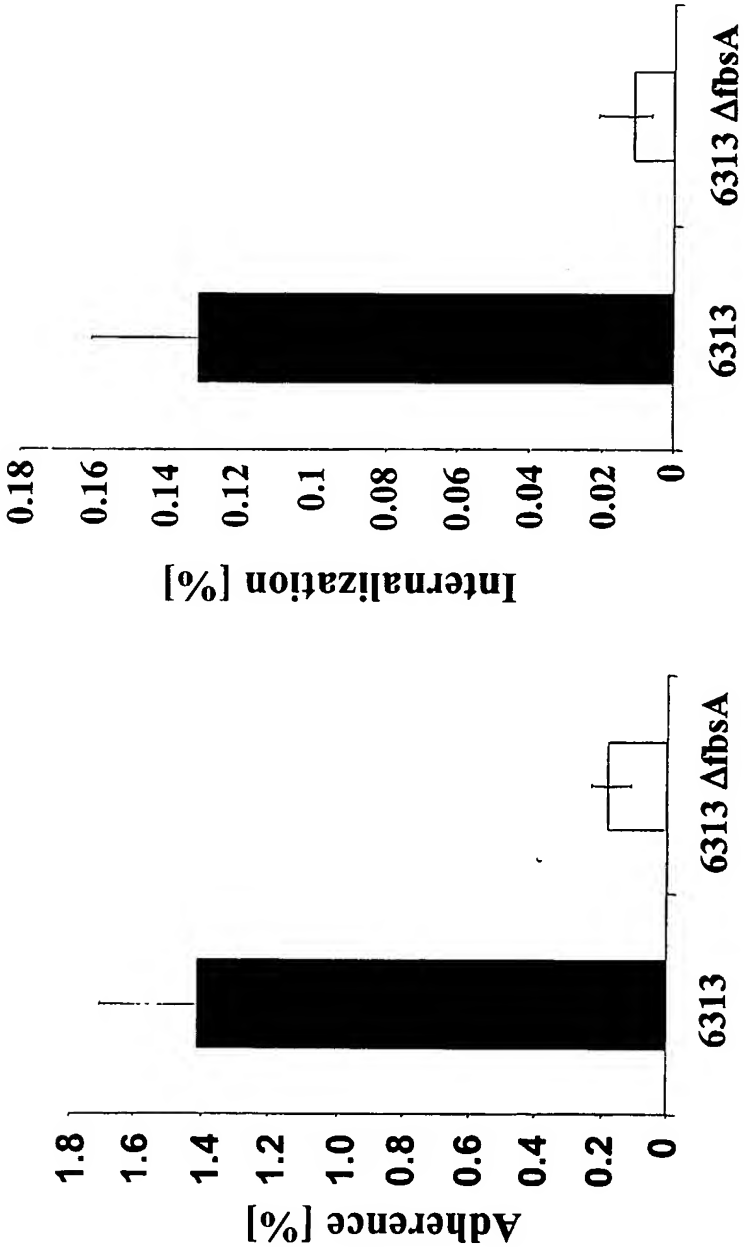

6313 ΔfbsA
6313
0.18
0.16
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
Internalization [%]
6313 ΔfbsA
6313
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0
Adherence [%]

Fig. 25

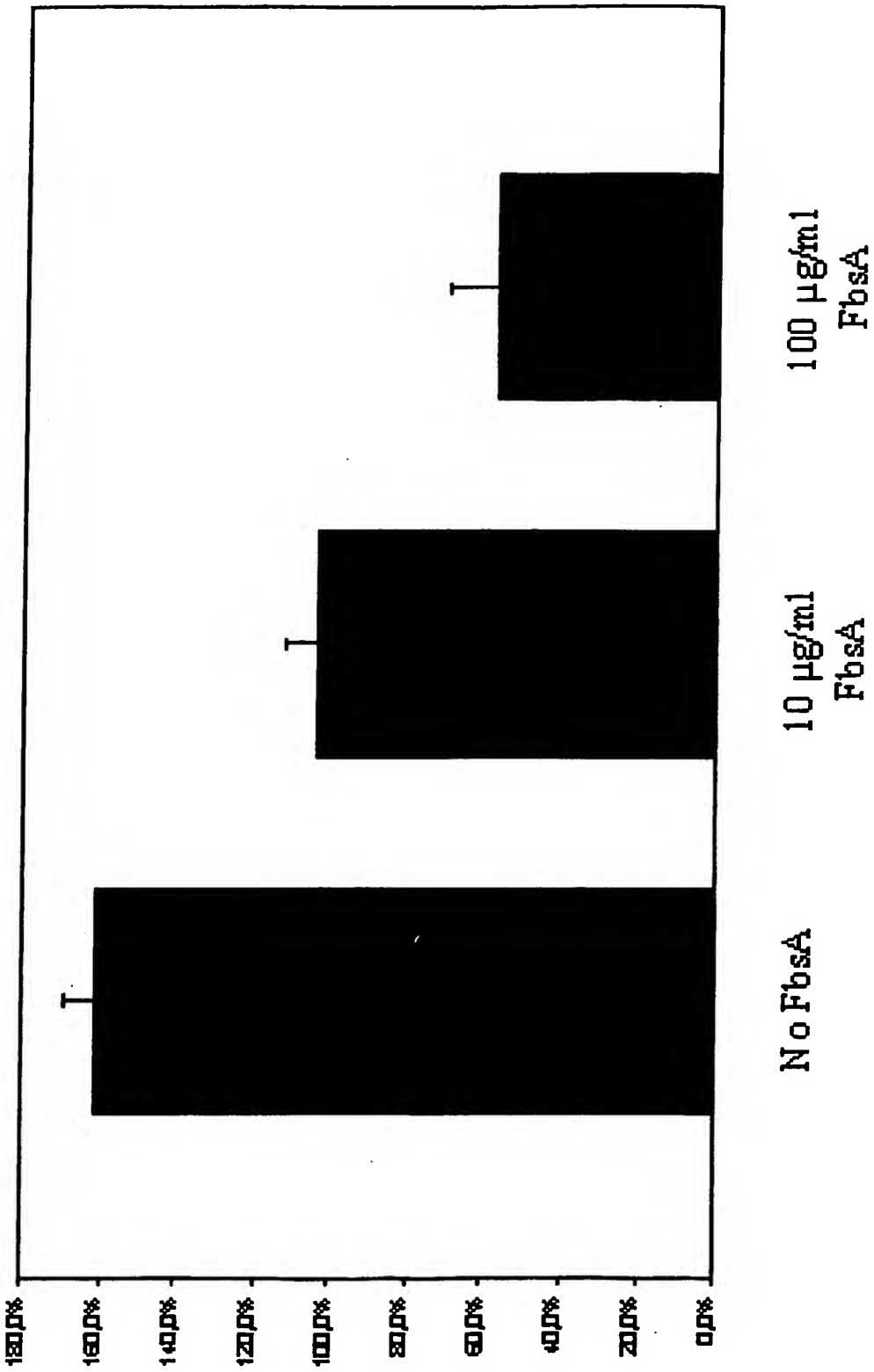

Adherence to A549 cells
0%
20%
40%
60%
80%
100%
120%
140%
160%
180%
No FbsA
10 µg/ml FbsA
100 µg/ml FbsA

Fig. 26

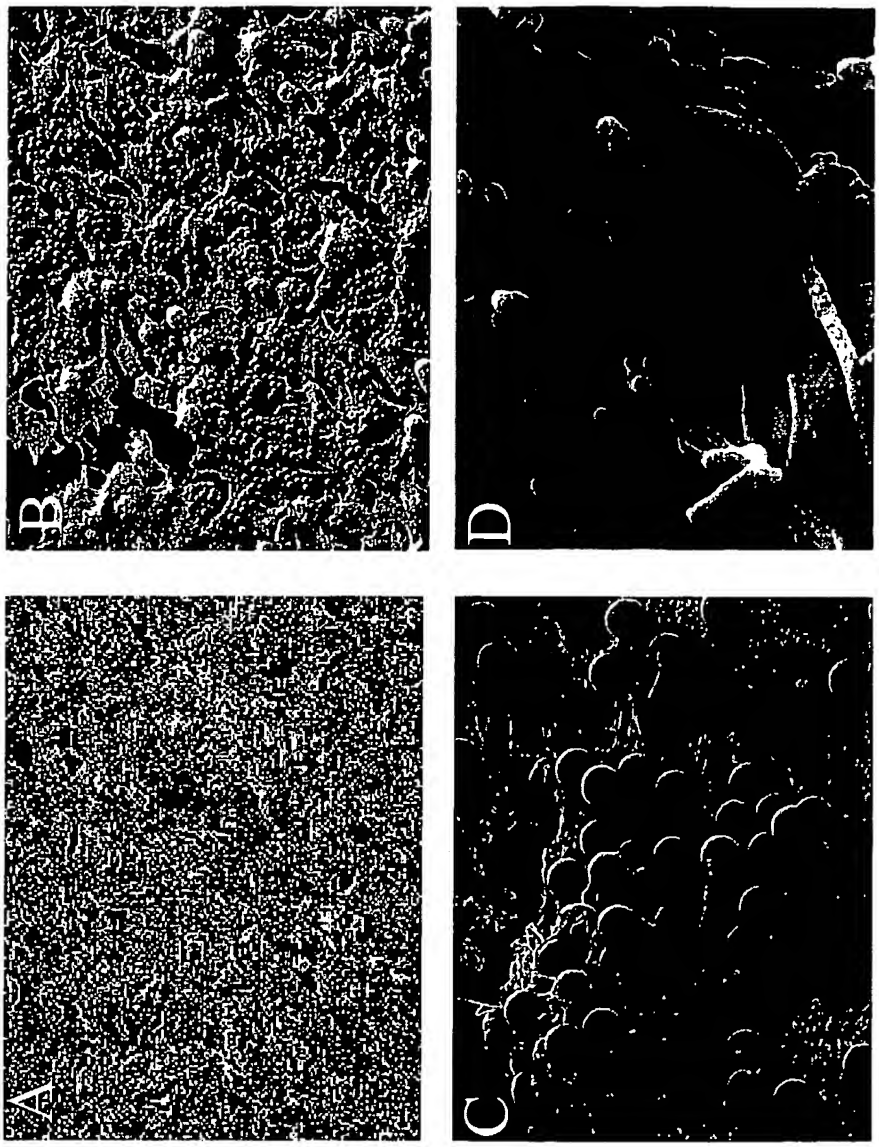


Fig. 27

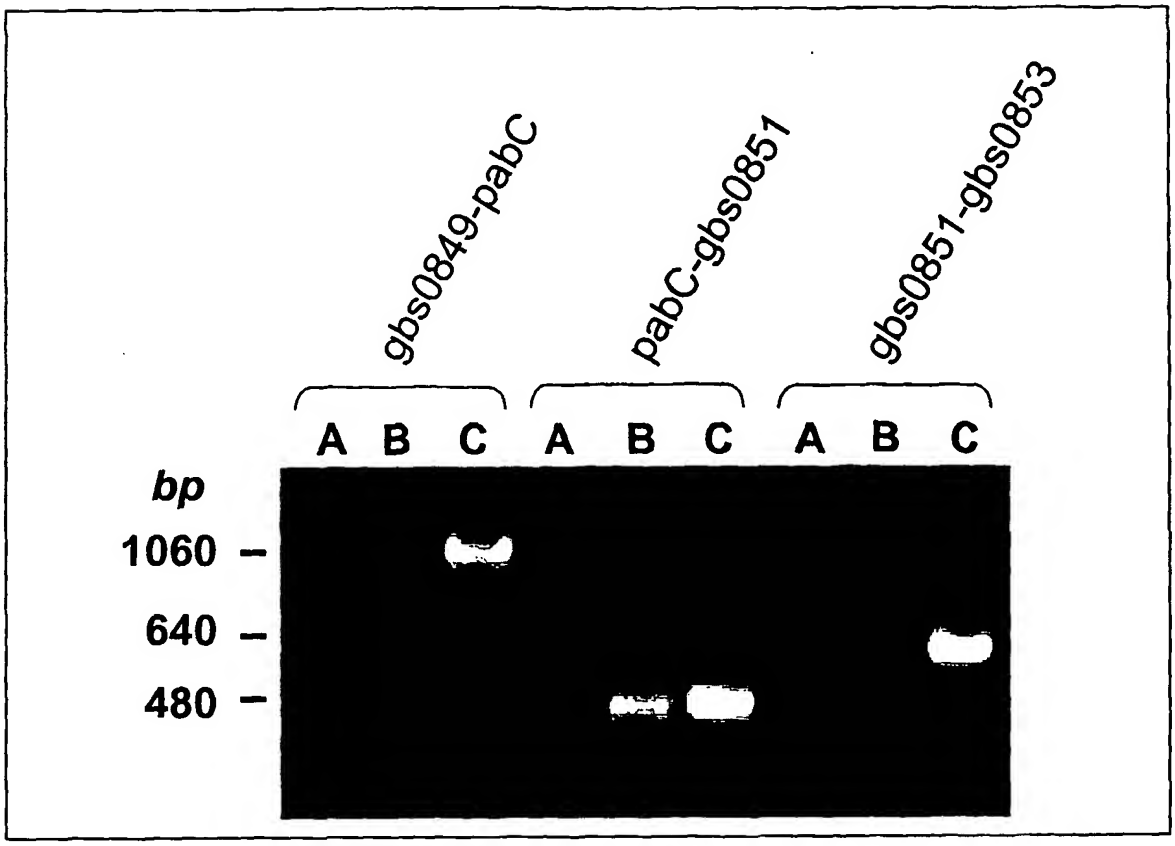

gbs0849-pabC
pabC-gbs0851
gbs0851-gbs0853
A B C A B C A B C
bp
1060
640
480

Fig. 28

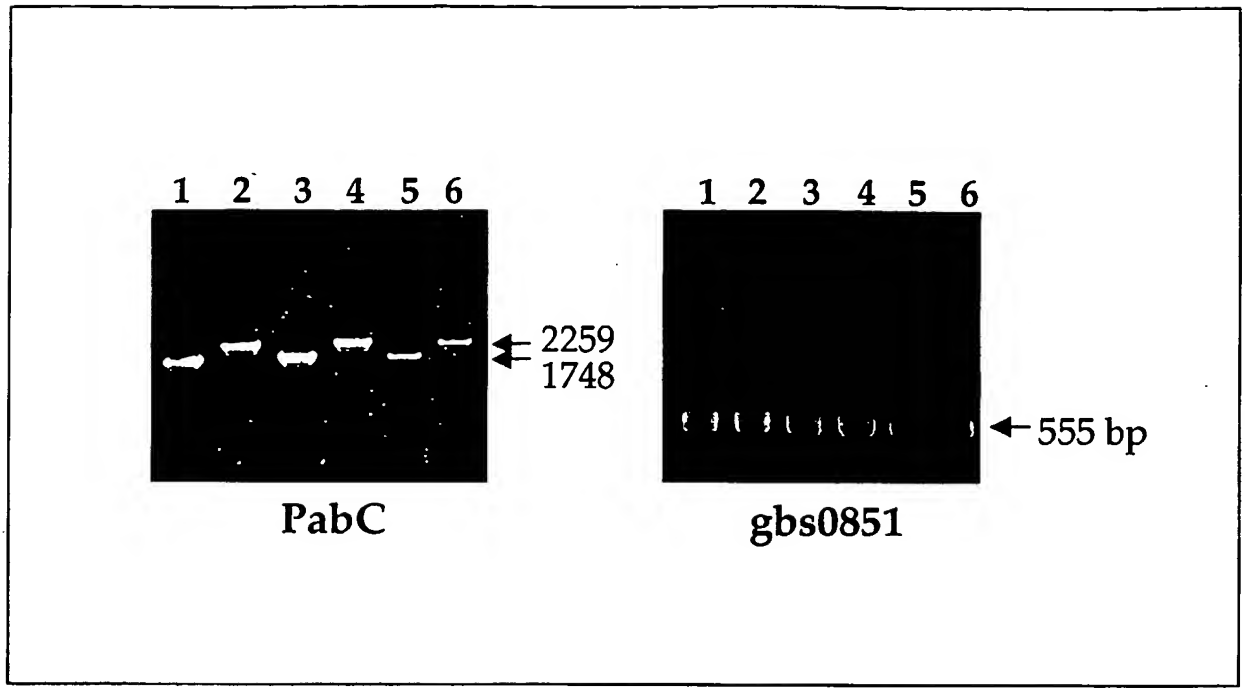


Fig. 29

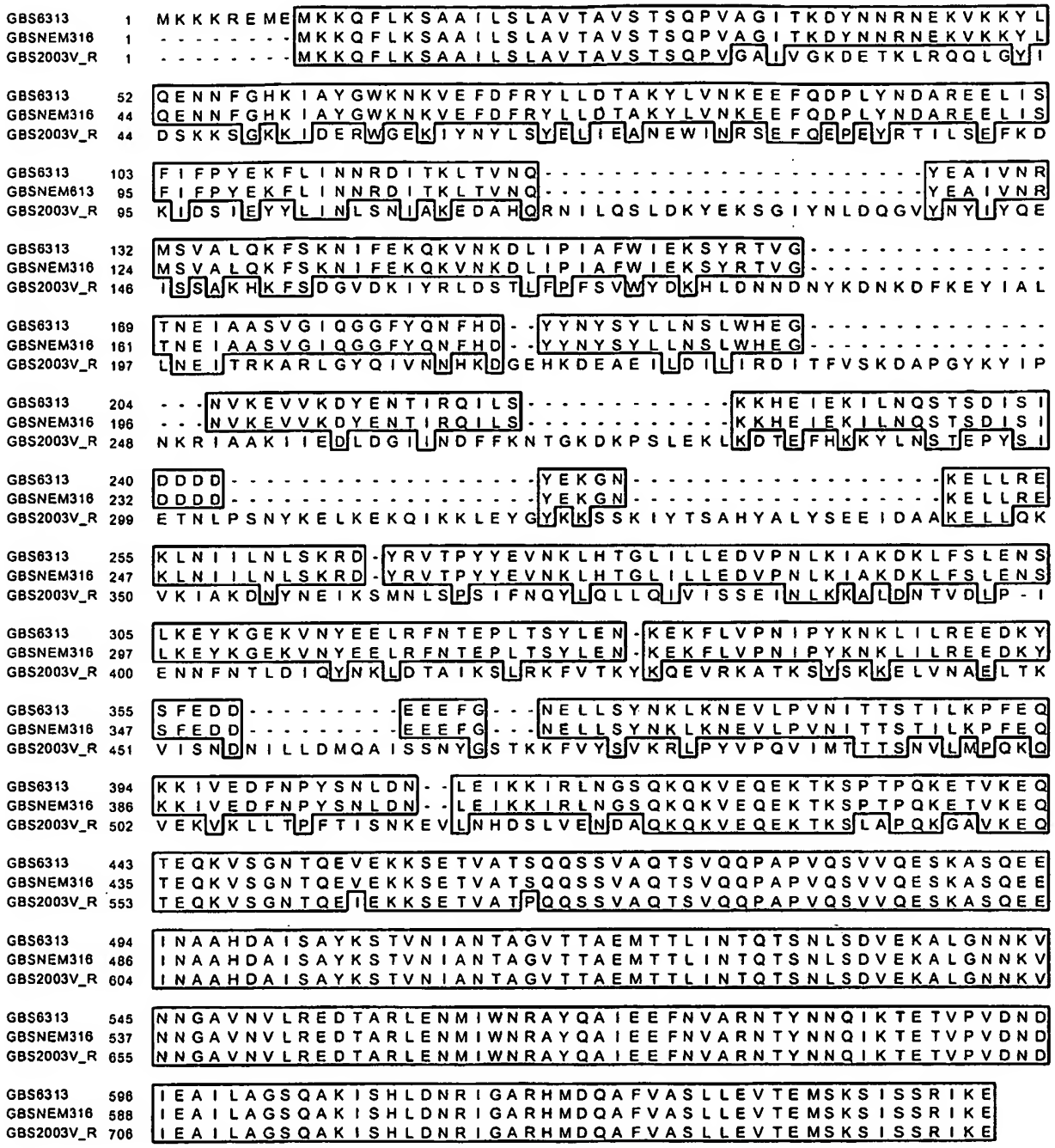
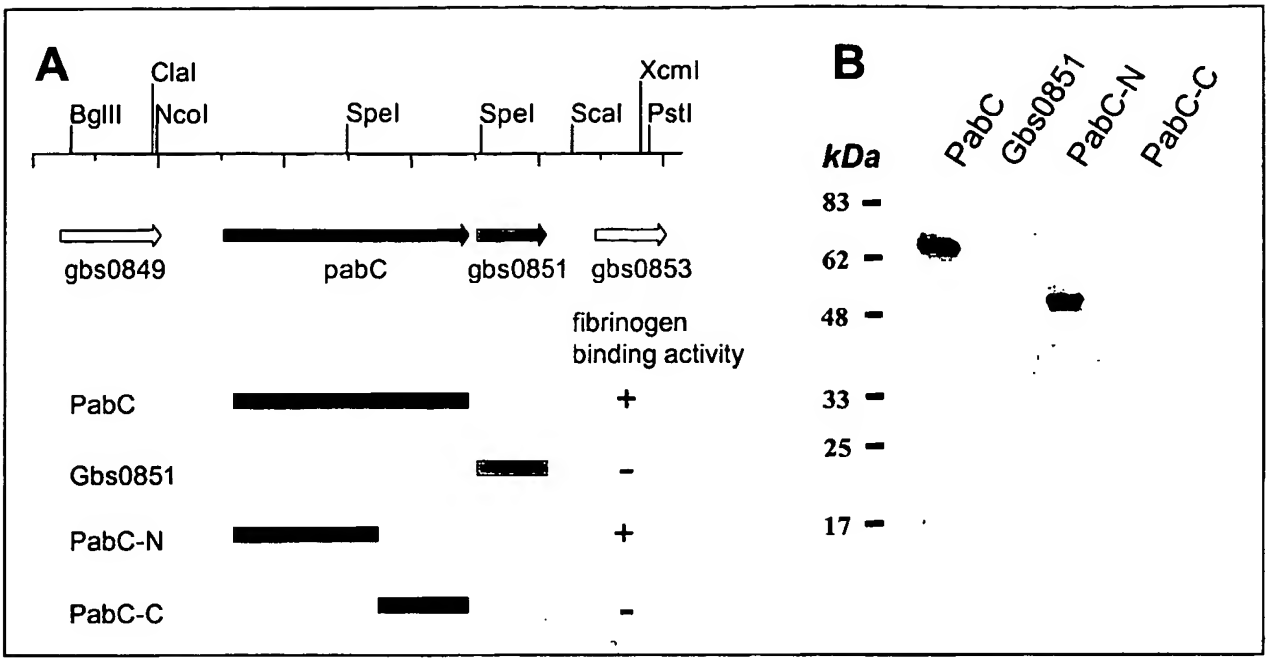

GBS6313 1 MKKKREMEMKKQFLKSAAILSLAVTAVSTSQPVAGITKDYNNRNEKVKKYL
GBSNEM316 1 ---------MKKQFLKSAAILSLAVTAVSTSQPVAGITKDYNNRNEKVKKYL
GBS2003V_R 1 ---------MKKQFLKSAAILSLAVTAVSTSQPVGAIVGKDETKLRQQLGYI
GBS6313 52 QENNFGHKIAYGWKNKVEFDFRYLLDTAKYLVNKEEFQDPLYNDAREELIS
GBSNEM316 44 QENNFGHKIAYGWKNKVEFDFRYLLDTAKYLVNKEEFQDPLYNDAREELIS
GBS2003V_R 44 DSKKSGKKIDERWGEKIYNYLSYELIEANEWINRSEFQEPEYRTILSEFKD
GBS6313 103 FIFPYEKFLINNRDITKLTVNQ----------YEAIVNR
GBSNEM613 95 FIFPYEKFLINNRDITKLTVNQ----------YEAIVNR
GBS2003V_R 95 KIDSIEYYLINLSNIAKEDAHQRNILQSLDKYEKSGIYNLDQGVYNYIYQE
GBS6313 132 MSVALQKFSKNIFEKQKVNKDLIPIAFWIEKSYRTVG----------
GBSNEM316 124 MSVALQKFSKNIFEKQKVNKDLIPIAFWIEKSYRTVG----------
GBS2003V_R 146 ISSAKHKFSDGVDKIYRLDSTLFPFSVWYDKHLDNNDNYKDNKDFKEYIAL
GBS6313 169 TNEIAASVGIQGGFYQNFHD--YYNYSYLLNSLWHEG----------
GBSNEM316 161 TNEIAASVGIQGGFYQNFHD--YYNYSYLLNSLWHEG----------
GBS2003V_R 197 LNEITRKARLGYQIVNNHKDGEHKDEAEILDILIRDITFVSKDAPGYKYIP
GBS6313 204 ---NVKEVVKDYENTIRQILS----------KKHEIEKILNQSTSDISI
GBSNEM316 196 ---NVKEVVKDYENTIRQILS----------KKHEIEKILNQSTSDISI
GBS2003V_R 248 NKRIAAKIIEDLDGILNDFFKNTGKDKPSLEKLKDTEFHKKYLNSTEPYSI
GBS6313 240 DDDD----------YEKGN----------KELLRE
GBSNEM316 232 DDDD----------YEKGN----------KELLRE
GBS2003V_R 299 ETNLPSNYKELKEKQIKKLEYGYKKSSKIYTSAHYALYSEEIDAAKELLQK
GBS6313 255 KLNIILNLSKRD-YRVTPYYEVNKLHTGLILLEDVPNLKIAKDKLFSLENS
GBSNEM316 247 KLNIILNLSKRD-YRVTPYYEVNKLHTGLILLEDVPNLKIAKDKLFSLENS
GBS2003V_R 350 VKIAKDNYNEIKSMNLSPSIFNQYLQLLQIVISSEINLKKALDNTVDLP-I
GBS6313 305 LKEYKGEKVNYEELRFNTEPLTSYLEN-KEKFLVPNIPYKNKLILREEDKY
GBSNEM316 297 LKEYKGEKVNYEELRFNTEPLTSYLEN-KEKFLVPNIPYKNKLILREEDKY
GBS2003V_R 400 ENNFNTLDIQYNKLDTAIKSLRKFVTKYKQEVRKATKSYSKKELVNAELTK
GBS6313 355 SFEDD---------EEEFG---NELLSYNKLKNEVLPVNITTSTILKPFEQ
GBSNEM316 347 SFEDD---------EEEFG---NELLSYNKLKNEVLPVNITTSTILKPFEQ
GBS2003V_R 451 VISNDNILLDMQAISSNYGSTKKFVYSVKRLPYVPQVIMTTTSNVLMPQKQ
GBS6313 394 KKIVEDFNPYSNLDN--LEIKKIRLNGSQKQKVEQEKTKSPTPQKETVKEQ
GBSNEM316 386 KKIVEDFNPYSNLDN--LEIKKIRLNGSQKQKVEQEKTKSPTPQKETVKEQ
GBS2003V_R 502 VEKVKLLTPFTISNKEVLNHDSLVENDAQKQKVEQEKTKSLAPQKGAVKEQ
GBS6313 443 TEQKVSGNTQEVEKKSETVATSQQSSVAQTSVQQPAPVQSVVQESKASQEE
GBSNEM316 435 TEQKVSGNTQEVEKKSETVATSQQSSVAQTSVQQPAPVQSVVQESKASQEE
GBS2003V_R 553 TEQKVSGNTQEIEKKSETVATPQQSSVAQTSVQQPAPVQSVVQESKASQEE
GBS6313 494 INAAHDAISAYKSTVNIANTAGVTTAEMTTLINTQTSNLSDVEKALGNNKV
GBSNEM316 486 INAAHDAISAYKSTVNIANTAGVTTAEMTTLINTQTSNLSDVEKALGNNKV
GBS2003V_R 604 INAAHDAISAYKSTVNIANTAGVTTAEMTTLINTQTSNLSDVEKALGNNKV
GBS6313 545 NNGAVNVLREDTARLENMIWNRAYQAIEEFNVARNTYNNQIKTETVPVDND
GBSNEM316 537 NNGAVNVLREDTARLENMIWNRAYQAIEEFNVARNTYNNQIKTETVPVDND
GBS2003V_R 655 NNGAVNVLREDTARLENMIWNRAYQAIEEFNVARNTYNNQIKTETVPVDND
GBS6313 596 IEAILAGSQAKISHLDNRIGARHMDQAFVASLLEVTEMSKSISSRIKE
GBSNEM316 588 IEAILAGSQAKISHLDNRIGARHMDQAFVASLLEVTEMSKSISSRIKE
GBS2003V_R 706 IEAILAGSQAKISHLDNRIGARHMDQAFVASLLEVTEMSKSISSRIKE

Fig. 30


A
ClaI
XcmI
BglII
NcoI
SpeI
SpeI
ScaI
PstI
gbs0849
pabC
gbs0851
gbs0853
fibrinogen binding activity
PabC
+
Gbs0851
-
PabC-N
+
PabC-C
-
B
kDa
PabC
Gbs0851
PabC-N
PabC-C
83
62
48
33
25
17

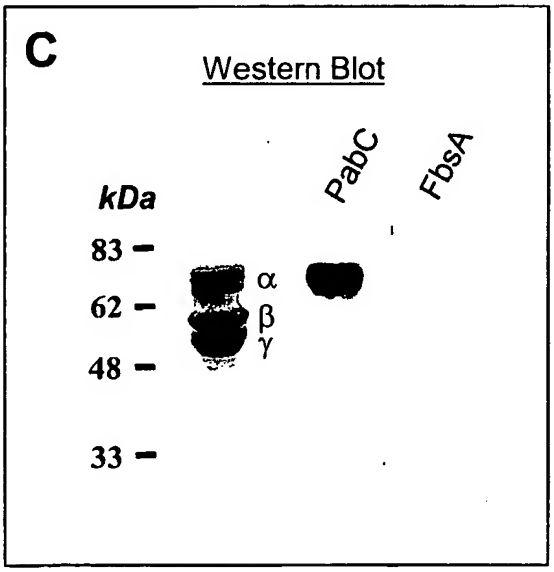

C
Western Blot
kDa
PabC
FbsA
83
62
48
33
α
β
γ

Fig. 31

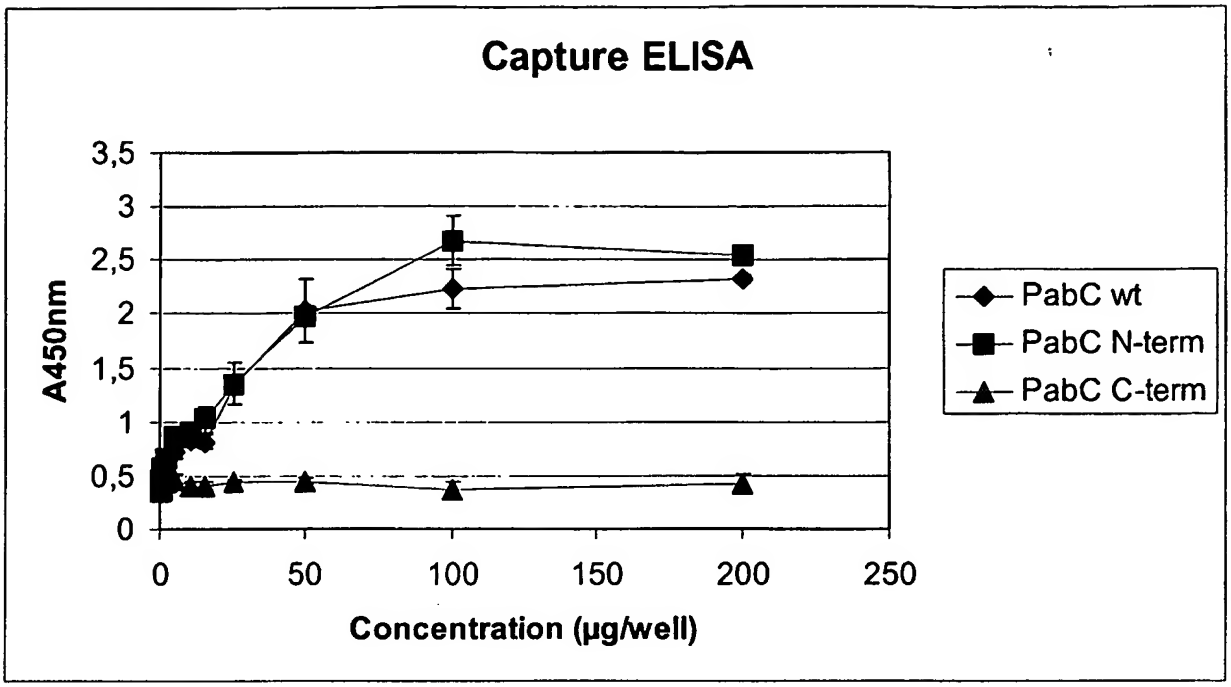
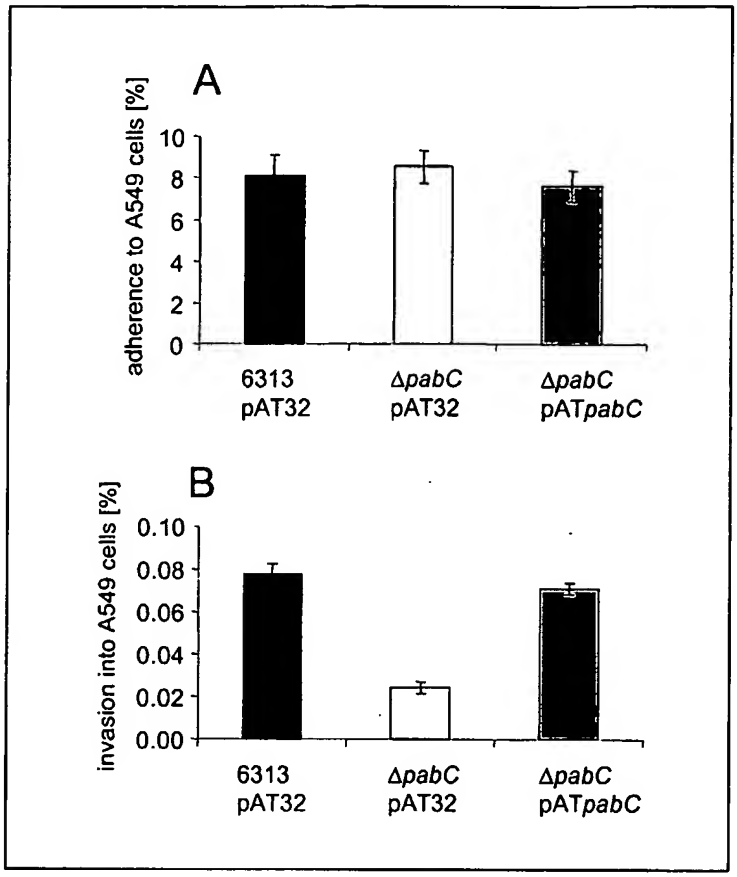

Capture ELISA
A450nm
3,5
3
2,5
2
1,5
1
0,5
0
0
50
100
150
200
250
Concentration (µg/well)
PabC wt
PabC N-term
PabC C-term

Fig. 32


A
adherence to A549 cells [%]
10
8
6
4
2
0
6313 pAT32
ΔpabC pAT32
ΔpabC pATpabC
B
invasion into A549 cells [%]
0.10
0.08
0.06
0.04
0.02
0.00
6313 pAT32
ΔpabC pAT32
ΔpabC pATpabC

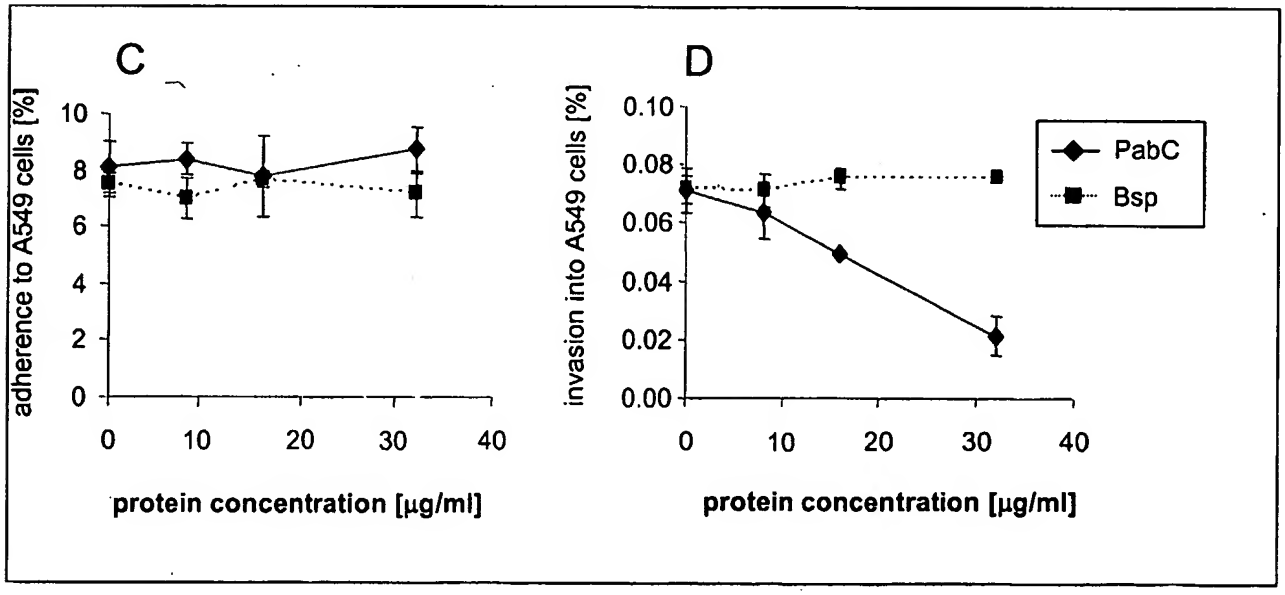

C
adherence to A549 cells [%]
10
8
6
4
2
0
0
10
20
30
40
protein concentration [µg/ml]
D
invasion into A549 cells [%]
0.10
0.08
0.06
0.04
0.02
0.00
0
10
20
30
40
protein concentration [µg/ml]
PabC
Bsp

Fig. 33